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Database :
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Perfect score:
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    Issued_Patents_NA:*
1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/2
3: /cgn2_6/ptodata/2
4: /cgn2_6/ptodata/2
5: /cgn2_6/ptodata/2
6: /cgn2_6/ptodata/2
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length: 2000000000
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Copyright (c) 1993 - 2000 Comp
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/Packfiles1.seq:*
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   3447
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US-08-313-185-59
US-09-082-614A-59
US-08-757-653-136
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US-08-757-653-140
US-08-757-653-140
US-08-757-653-140
US-08-757-653-140
US-08-757-053-140
US-08-757-084A-71
US-08-750-084A-71
US-08-750-084A-71
US-08-750-084A-71
US-08-750-084A-71
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US-08-906-769-169
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US-08-906-614-171
US-08-906-614-171
US-08-906-616-171
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US-08-906-759-171
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33.266 Million cell updates/sec
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59, Appl
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RESULT US-08 VS-08	000 00 0 00
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1 1 185-59/c ance 59, Appli it No. 585163 EAAL INFORMATI PPLICANT: Col PPLICANT: Col PPLICANT: You PPLICANT: You PPLICANT: Tel PADDRESSEE: F ADDRESSEE: F ADDRESSEE: F ADDRESSEE: D COUNTRY: Washin STATE: D.C. CITY: Washin STATE: D.C. COUNTRY: Usahin STATE: D.C. COUNTER READAB MEDIUM TYPE: COMPUTER: LB OPERATION NEDIUM TYPE: COMPUTER: PA FRENT APPLICATION REFERENCE CAADAB APPLICATION REFERENCE CHARAC LENGTH: 432 TYPE: nucle: TSTRANDEDNESS: 130-185-59	11222112331133
T 1 -313-185-59/c uence 59, Application US/08313 ent No. 5851763. NERAL INFORMATION: APPLICANT: Heym, Beate APPLICANT: Cole, Stewart APPLICANT: Zohng, Ying APPLICANT: Zohng, Ying APPLICANT: Telenti, Amalio APPLICANT: Bodmer, Thomas TITLE OF INVENTION: Rapid Det TITLE OF INVENTION: ASSISTEM: PC-DOS/MS COMPUTER: ISM PC Compatible OPERATION SYSTEM: PC-DOS/MS SOFTWARE: PatentIn Release CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US/08/3 FILING DATE: 12-OCT-194 CLASSIFICATION NUMBER: US/08/3 FILING DATE: 12-OCT-194 CLASSIFICATION NUMBER: 05/08/3 FILING DATE: 12-OCT-194 CLASSIFICATION INFORMATION: REGISTRATION NUMBER: 05/08/3 FILING DATE: 12-OCT-194 CLASSIFICATION INFORMATION: REGISTRATION INFORMATION: REGISTRATION INFORMATION: TELEPHONE: (202) 408-44000 TELEFAX: (202) 408-44000	660.0000000000000000000000000000000000
	537 1938 1938 1938 3000 3000 3021 3217 412 412 645 645 645 645 645 709 709
us/0831318 e e art glas g glas g glas g g glas g g g las malio omas n Mycobact 66 c-Dos/Ms-D Release #1 TION: th J. 1994 TION: th J. 55: 68-87000 0: 59: 68-87000 0: 59: 68-87000 0: 59: 65: 65: 65: 65: 65: 65: 65: 65: 65: 65	44444444444444444444444444444444444444
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Resistance	Sequence 171. Sequence 29, Sequence 29, Sequence 1, Sequence 1, Sequence 64, Sequence 64, Sequence 64, Sequence 6, Sequence 1, Sequence 1, Sequence 1, Sequence 2, Sequence 1, Sequence 2, Sequence 12, Sequence 12, Sequence 20, Sequence 4, Sequence 4, Sequence 20, Sequence 20, Sequence 615
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Query Match

100.0%;

Score

20; DB 2;

Length 432;

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Best Local Similarity Matches 20; Conserv

100.0%;

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RESULT 3
US-08-757-653-135/c
                       Sequence
Patent No
                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: US-09-082-614A-59
                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleib acid
STRANDEDNESS:
                                                                                                                                                                                               Matches
                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

APPLICATION NUMBER: US/09/082,614A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 12-OCT-1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance TITLE OF INVENTION: in Mycobacterium Tuberculosis NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                             Local
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REFERENCE/DOCKET NUMBER: 02356.0068-00000
                         No.
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                         135, Application US/08757653
5. 5843669
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Similarity 100.0%;
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Telenti, Amalio
Bodmer, Thomas
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Cole, Stewart
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Zhang, Ying
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Pred. No. 0.00054;
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LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomi
US-08-757-653-135
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Patent No. 5843669
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Best Local
                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                        APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ingolia, Diane E. 027 REGISTRATION NUMBER: 40,027 REFERENCE/DOCKET NUMBER: FOI TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: THE POPPY DISK
COMPUTER: THE POPPY DISK
COMPUTER: PATENT PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                   296 TACGGCGTTTCGATGAACCC 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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STATE: California
COUNTRY: United States Of America
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                                                                                                               United States Of America
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Pred. No. 0.00054;
Mismatches 0;
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Length 620; Indels

0,

Gaps

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FILING DATE:

APPLICATION NUMBER: US/08/757,653

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; MOLECULE TYPE: US-08-757-653-137
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Patent No. 5843669
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INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
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Best Local (
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                                                                                                   TELEFAX: (415) 397-833
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                   REFERENCE/DOCKET NUMBER: FO TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,0
                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
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ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                              TYPE: nucleic acid
STRANDEDNESS: doub
                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94104
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Local Similarity 100.0%;
les 20; Conservative 0
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                                                                                 620 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                           United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (415) 705-8410
              DNA (genomic)
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                                                 double
                                                                                                                                        397-8338
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                                                                                                                                                                                                         40,027
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Pred. No. 0.00054;
); Mismatches 0;
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US-08-757-653-139
; Sequence 139, Application US/08757653
; Patent No. 5843669
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                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
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                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kaiser, Machine I.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
APPLICANT: Lyamichev, Natasha
APPLICANT: Cleavage Of Nucleic Acid Using
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: FC TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                      325 TACGGCGTTTCGATGAACCC 344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296 TACGGCGTTTCGATGAACCC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Ingolia, Diane E. REGISTRATION NUMBER: 40,027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
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5. 5843669
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T: 220 Montgomery Street, Suite
San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleic acid
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Pred. No. 0.00054;
); Mismatches 0;
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Pred. No. 0.00054;
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                                                                                                                                                                                                                                                                                                                      Length 620;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 584300;
Patent No. 584300;
Patent INFORMATION;
Paiser
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REFERENCE/DOCKET NUMBER: FORS-02565
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHONE: (415) 397-8338
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
                                              ATTORNEY/AGENT INFORMATION: NAME: Ingolia, Diane F
                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FO
                                                                                             APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                ADDRESSEE: Medlen & Carrott, Line STREET: 220 Montgomery Street, Suite 2200 CITY: San Francisco STATE: California COUNTRY: United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                          CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       325 TACGGCGTTTCGATGAACCC 344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: BATCHTE PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 220 Montgome CITY: San Francisco STATE: California
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5843669
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FORS-02565
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Pred. No.
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US-08-797-812-24/c
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Patent No.
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REFERENCE/DOCKET NUMBER: 16:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEPAX: 415-326-2422
                                                                                                       PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/011,339
PTITNE DATE: 08-FEB-1996
                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/017,765
FILING DATE: 15-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/629,031
FILING DATE: 08-APR-1996
                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,631
FILING DATE: 01-MAR-1996
                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYDE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy |
COMPUTER: IBM PC COM
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LENGTH: 620 base pairs
TYPE: nucleic acid
STRANNEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP STREET: Two Embarcadero Center, 8th Floor CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Chip-Based Species Identification and TITLE OF INVENTION: Phenotypic Characterization of Microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: CA
COUNTRY: US
ZIP: 94111
                                                                    NAME: Fitts, Renee A. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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6228575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berno, Anthony J.
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Chee, Mark S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stryer, Lubert
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                                                                                                                                                                                                                                                                                                                                  UMBER: US/08/797,812
07-FEB-1997
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Pred. No.
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130:219116
      Method of selecting PCR primer pairs to amplify a group of related
      nucleotide sequences
 IN
      McClelland, Michael; Pesole, Graziano
 PA
      Sidney Kimmel Cancer Center, USA
 SO
      PCT Int. Appl., 92 pp.
      CODEN: PIXXD2
 DΤ
      Patent
LΑ
      English
FAN.CNT 1
      PATENT NO.
                         KIND
                               DATE
                                                APPLICATION NO.
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PΙ
      WO 9911823
                         A2
                                19990311
                                                WO 1998-US18392 19980904
      WO 9911823
                         A3
                                19990610
          W: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE,
               DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG,
               KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX,
              NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, AM, AZ, BY, KG, KZ, MD, RU, TJ, TM
          RW: GH, GM, KE, LS, MW, SD, SZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI,
              CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
     AU 9893027
                         A1
                             19990322
                                               AU 1998-93027
                                                                   19980904
     EP 1007739
                         A2
                               20000614
                                               EP 1998-945882
                                                                   19980904
             AT, BE, CH, DE, DK, ES, FR, GB, GR, IT, LI, LU, NL, SE, MC, PT,
              IE, FI
PRAI US 1997-925816
                         Α
                               19970905
     WO 1998-US18392
                         W
                               19980904
     The present invention provides a method of detg. a set of primer pairs for
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amplifying a group of related nucleotide sequences. A method of the invention is performed by identifying a group of related nucleotide sequences; generating the set of primers that matches each of the related nucleotide sequences; detg. for each systematic pairing of each primer which of the related nucleotide sequences are amplified; and selecting from the systematic pairings a subset which amplifies all of the related nucleotide sequences. The invention also provides a method of using a set of primer pairs, which amplify a group of related nucleotide sequences, to identify nucleotide sequences related to the original group of nucleotide sequences. Eight-mer primer pairs are provided for amplification of genes encoding nuclear receptors, G-protein coupled receptors, apoptosis-assocd. proteins, DNA repair enzymes, and replication enzymes. The invention also provides a computer app. for carrying out the computer-executed steps of the method. The invention further provides a computer program product comprising a signal bearing media for carrying out the method.

GENERAL INFORMATION:

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RESULT 11
PCT-US95-06790-1/c
; Sequence 1, Application PC/TUS9506790
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Best Local Similarity
                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                             TELEFAX: 612-39-30131
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection
TITLE OF INVENTION: Resistance
TITLE OF INVENTION: Clinical:
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: 612-339-0331
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LENGTH: 706 base pairs
                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA
                                                                                           671 TACGGCGTTTCGATGAACCC 652
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                                                                                                                                                           y Match 100.0%;
Local Similarity 100.0%;
hes 20; Conservative 0;
                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/0 FILING DATE: 26-MAY-1994
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TOPOLOGY: 11r
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                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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                                                                                                           1 tacggcgtttcgatgaaccc 20
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3500 IDS Center
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hes 0;
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                                                                                                                                                                                          Length 970;
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US-08-750-088A-71
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Rasch, Kevin W.
REGISTRATION UNMBER: 35,651
REFERENCE/DOCKET NUMBER: 150
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEPAX: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                     APPLICANT: JANNES, GI
APPLICANT: ROSSAU, RI
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                            APPLICANT:
APPLICANT:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: 1: MOLECULE TYPE:
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                                                                                                                                                STREET: 1100 NEW CITY: WASHINGTON
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                                                                                                              COUNTRY: US
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                                                                                                                                                                                                                                                                                                                                                                                   1, Application US/08750088A 6329138
                                                                                               20005-3934
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1100 NEW YORK AVENUE, SUITE 600
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3500 IDS Center
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                                                                                                                                                                                                                                                                           ROSSAU, RUDI
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PORTAELS, FRAN OISE
MACHTELINCKX, LIEVE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                       METHOD FOR DETECTION OF THE ANTIBIOTIC RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES: 71
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Pred. No. 0.00053;
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CURRENT APPLICATION DATA:

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US-08-250-030-9
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US-08-250-030-9
                                                        TELEPAX: 612-335 CT.
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TENGTH: 27 base pairs
TENGTH: 27 base pairs
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 9, Application US/08250030 Patent No. 5643723
                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: MUETING, ANN M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 150.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
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INFORMATION FOR SEQ ID NO: 71:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION UMBER: US/08/250,030
FILING DATE: 26-MAY-1994
             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection
TITLE OF INVENTION: Resistan
TITLE OF INVENTION: Clinical
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TELEPHONE: 202-371-2540
TELEFAX: 202-371-2540
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                                         STRANDEDNESS:
                          TOPOLOGY:
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TOPOLOGY: lin
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)N: 435
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100.0%; Pr
0;
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Resistance to Rifampin in Mycobacterial Cultures and
Clinical Specimens
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                                                                                                                                                                 150.105US1
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Pred. No.
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0.0024;
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RESULT 15
US-08-313-185-57/c
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TELEPAX: 612-339-3061
TELEPAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
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                                                                                                                                                      Sequence 57, Application US/08313185 Patent No. 5851763
                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                       Query Match 75.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 9, Application PC/TUS9506790 GENERAL INFORMATION:
                                                      APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
                                                                                                                                      GENERAL INFORMATION:
   APPLICANT: Young, Douglas APPLICANT: Zhang, Ying APPLICANT: Honore, Nadine APPLICANT: Telenti, Amalio APPLICANT: Bodmer, Thomas TITLE OF INVENTION: Rapid D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Radsch, Kevin W.
REGISTRACION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION: NAME: Raasch, Kevin W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Mayo Foundation for Medical Education and Research APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding TITLE OF INVENTION: Resistance to Rifampin
                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
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TOPOLOGY: lir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 26-MA' CLASSIFICATION:
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                                                                                                                                                                                                                                                         1 CGTTTCGATGAACCC 15
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STREET: 3500 IDS Center
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Rapid Detection of Antibiotic Resistance
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NUMBER OF INVENTION: 1n Mycobacterium Tuberculosis

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:
ADDRESSE: Pinnegan, Henderson, Farabow, Garrett & ADDRESSE: Dunner

STREET: 1300 I Street, N.W.
CITY: Washington
CITY: Washington
STATE: D.C.
COUNTRY: USA
IP: 20005-313:
COMPUTER ENDABLE FORM:
MEDIUM TYPE: PLOPY disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/313/185

FILING DATE: 10-COT-1994

CLASSIFICATION NUMBER: US/08/313/185
FILING DATE: 10-COT-1994

CLASSIFICATION NUMBER: 25/146
REFERENCE/DOCKET NUMBER: 25/146
REFERENCE/DOCKET NUMBER: 25/146
REFERENCE/DOCKET NUMBER: 25/16
REFERENCE/ATION NUMBER: 25/16
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length: 2000000000
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| SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
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Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                                                                                                             the number of results predicted by chance to have a r than or equal to the score of the result being printed, ed by analysis of the total score distribution.
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ABL14021 AAS54170 ABL14020 AA199683 AA199682 AAV31045	AAX27183 AAX27183 AAX27186 AAX27186 AAS99557 AAS99565 AAS99565 AAS99568 AAS9568 AAS95584	AA061457 AAA49863 AAT109676 AAH51976 AAH72179 AAA74651 AAA89991 AAA727217 AAS59653 AAT12091 AAC8922 AAX27112 AAX27113 AAX27118 AAX27119 AAX27119 AAX27117 AAX27104 AAX27117	AAS99530 AAS99531
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ALIGNMENTS

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RESULT 1
AAT12092
ID AAT12092 standard; DNA;
                                                                                                                                                               Antiblotic; resistance; spectrum; gene; mycobacterium; determination; amplification; tuberculosis; rpoB; fragmen primer; differential; hybridisation; pattern; rifampicin; rifabutin; species identification; ss.
      WPI; 1996-040250/04
                                                                                       09-JUN-1995;
                                                                                                          14-DEC-1995
                                                                                                                        WO9538851-A2
                                                                                                                                              Synthetic
                                                                                                                                                                                                             M. tuberculosis rpoB gene fragment amplification primer P2
                         Rossau R;
                                  De Beenhouwer H,
                                                   (INNO-) INNOGENETICS NV.
                                                                       09-JUN-1994;
                                                                                                                                                                                                                                10-JUL-1996
                                                                                                                                                                                                                                                   AAT12092;
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                                                                       94EP-0870093
                                                                                       95WO-EP02230
                                  Jannes
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                                 Machtelinckx L,
                                                                                                                                                                                 tuberculosis; rpoB; fragment;
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Mycobacterium Mycobacterium

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RESULT
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Best Local S
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The present sequence is that of the Mycobacterium tuberculosis rpoB (rifampin resistance) gene amplification primer rpoB-F (bp 2201-2220). It is used with the reverse primer given in AAA49824 and with the sequencing primers given in AAA49825 and AAA49826 for the detection and analysis of antibiotic resistance-associated mutations of the rpoB gene (see AAA49863). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
                                                                                                                                                                                                                                                                                                        WPI;
                                                                                                                                                                                                                                   Method for the detection and characterization of Mycobacterium tuberculosis with antibiotic resistance in a sample - \,
                                                                                                                                                                                                                                                                                                                                                                                                                  11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                         (VISI-) VISIBLE GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      10-DEC-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                      2000-431611/37
                                                                                                                                                                                                             4;
                                                                                                                                                                                                     Page 4; 43pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tuberculosis rpoB gene amplification primer rpoB-F.
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rpoB (rifampin resistance) gene sequencing primer rpoB-5s (bp 200-2220). It is used with the reverse primer given in AAA49826 and with the amplification primers given in AAA49824 for the detection and analysis of antibiotic resistance-associated mutations of the rpoB gene (see AAA4983). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR (isoniazid), mabA (isoniazid), rpsL/sl2 (streptomycin), kB/rrs (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.

Claim 4; Page

5; 43pp; English.

present sequence is that of the Mycobacterium tuberculosis

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Best Local
                                                                                                                                                  Method for the detection and characterization of Mycobacterium tuberculosis with antibiotic resistance in a sample - \,
                                                                                                                                                                                         WPI; 2000-431611/37.
                                                                                                                                                                                                                                                       11-DEC-1998;
                                                                                                                                                                                                                                 (VISI-) VISIBLE GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis rpoB gene sequencing primer
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                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis
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                      This sequence represents a mycobacterial rpoB gene fragment, that is amplified using the PCR primers of the invention. The primers form a method of detecting and identifying mycobacterial species by constructing a phylogenetic tree for the species. The use of the primers for sequence-specific amplification of the rpoB gene (encoding the beta subunit of RNA polymerase) from mycobacterial species provides an efficient way of characterising these species. In addition to phylogenetic analysis, the rpoB gene can be used as an alternative to the 16s rRNA gene because it has four subunits, which are highly conserved throughout prokaryotes. The method is particularly useful for slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              New pair of polymerase chain reaction (PCR) primers - for sequence-specific amplification of the rpoB gene from mycobacterial species, useful for detecting and identifying mycobacterial species
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llarity 100.0%;
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                               RpoB gene; mycobacteria; phylogenetic tree construction; mycobacterial species identification; phylogenetic analysis; ss
                                                                             RpoB gene fragment.
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            Mycobacteria bovis
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                                                                                                                                                                                                                                                                                            0.025;
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Best Local S
Matches 20
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         Kim H,
                                                                                                                                                                                                    Drug resistance oligonucleotide
                                                         30-MAY-2000; 2000KR-0029369
                                                                                                                                       WO200192573-A1
                                                                                30-MAY-2001; 2001WO-KR00904
                                                                                                                                                               Mycobacterium tuberculosis.
                                                                                                                                                                                                                                      Mycobacterium species identification primer #1.
                                                                                                                                                                                                                                                                      12-MAR-2002
                                                                                                                                                                                                                                                                                              AAS99526;
                                                                                                                                                                                                                                                                                                                      AAS99526 standard; DNA; 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 306 BP; 56 A; 95 C; 108 G; 47 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          susceptibility can be simultaneously determined in M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New pair of polymerase chain reaction (PCR) primers - for sequence-specific amplification of the rpoB gene from mycobacterial species, useful for detecting and identifying mycobacterial species
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         Kim N,
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                                                                                                                                                                                                                                                                  (first entry)
      Yoon S,
                                                                                                                                                                                              detection; mycobacterial species identification; probe; chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
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                              Kit for mycobacterial species identification and drug resistance detection, has oligonucleotide chip with species identification probacterial drug-resistance detection probe, and its contras
                                                                                                                                                                                                                                                                                                           Drug resistance oligonucleotide
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                                                                                                              Kia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  it for mycobacterial species identification and drug resistance etection, has oligonucleotide chip with species identification probe, mycobacterial drug-resistance detection probe, and its contrast grounds.
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                                                                                                             Kim N,
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                                                                                                                                                                2000KR-0029369
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                                                                                                                                                                                        2001WO-KR00904.
                                                                                                                                                                                                                                                                                                                                               species identification primer #2.
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                                                                                                                                                                                                                                                                                                         detection;
chip; rpoB
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                                                                                                                                                                                                                                                                                                         mycobacterial species identification; probe;
; sputum; blood; cerebrospinal fluid; ss;
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Pred. No. 0.0
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Disclosure;

Page 21;

corresponding to each drug resistance detection probe, and a marker detecting a hybridisation of the oligonucleotide chip and a specimer identification probe is comprised of species-specific DNA sequences

a specimen. To

probe

for

identification and drug resistance detection comprising an oligonucleotide chip including a species identification probe, a mycobacterial drug-resistance detection probe, a contrast group

The invention relates to a diagnostic kit for mycobacterial species

Disclosure;

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21; 74pp;

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Matches 20
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                                                                                                                                          Kit for mycobacterial species identification and detection, has oligonucleotide chip with species a mycobacterial drug-resistance detection probe,
                                                                                                                                                                                                                                                                                                                                                                                                                               Drug resistance 
oligonucleotide
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                                                                                                                                                                                                                                                     (BIOM-)
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chip; rpoB; sputum; blood; cerebrospinal fluid; ;
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             The invention relates to a diagnostic kit for mycobacterial species identification and drug resistance detection comprising an oligonucleotide chip including a species identification probe, a mycobacterial drug-resistance detection probe a contrast group probe corresponding to each drug resistance detection probe, and a marker for detecting a hybridisation of the oligonucleotide chip and a specimen. The identification probe is comprised of species-specific DNA sequences of mycobacterial rpoB gene and the detection probe is comprised of one or more modified codons of mycobacterial rpoB gene. The method involves amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction (PCR) and discriminating species by fluorescent intensity corresponding blood or cereborospinal fluid of a patient. Sequences AAS9478-AAS99569
                                                                                                                                                                                                                                                          Kit for mycobacterial species identification and drug resistance detection, has oligonuclectide chip with species identification | a mycobacterial drug-resistance detection probe, and its contras
                                                                                                                                                                                                                         Disclosure; Page 21; 74pp;
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chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
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20

Query Match Best Local S Matches 20

Similarity

100.0%;

Conservative

0;

Score 20; DB Pred. No. 0.0; Mismatches

0.025;

0,

0

Gaps

0;

DB

14;

Length 432; Indels

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AAQ61457
                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
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                   PCR amplification was used to obtain rpoB genes from rifamplcin-resistant Mycobacterium leprae strains. A comparison with the sequence of the rpoB gene from sensitive strains (AAQ51532) reveamutations in the region encoding amino acids 400-450. The correspondant was isolated from M.tuberculosis (AAQ61457). A common mutation seen in resistant strains occurs at codon 425 where Ser
                 substituted, m
                                                                                                                                                                                                                               17-SEP-1992;
30-APR-1992;
14-AUG-1992;
16-APR-1993;
  Sequence 432
                                                                                             Rapid detection of antibiotic resistance in Mycobacteria isoniazid, rifampicin or streptomycin resistance in tuber by detecting mutation in katG, rpoB or rpsL genes
                                                                              Example 2; Fig 13; 97pp; English.
                                                                                                                                                       Young
                                                                                                                                                                                        (MEDI-)
                                                                                                                                                                                                               (ASSI-)
                                                                                                                                                                                                                                                                        30-APR-1993;
                                                                                                                                                                                                                                                                                                                                                             M.tuberculosis
                                                                                                                                                                                                        (INSP)
                                                                                                                                                                                                                                                                                       11-NOV-1993
                                                                                                                                                                                                                                                                                                                      Mycobacterium
                                                                                                                                                                                                                                                                                                                                       mutant;
                                                                                                                                                                                                                                                                                                                                             rifampicin;
                                                                                                                                                                                                                                                                                                                                                                             17-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                              AAQ61457;
                                                                                                                                                                                                                                                                                                                                                                                                            AAQ61457 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               12
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DB; AAR51372.
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                                                                                                                                                                                                MEDICAL
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                                                                                                                                                       Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306
                                                                                                                                                                Cole
  ВP;
                                                                                                                                                                                                                                                                                                                                         antibiotic; susceptibility; sensitive; resistant; rpoB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP;
                                                                                                                                                                                                                              92FR-0011098.
92US-0875940.
92US-0929206.
93FR-0004545.
                                                                                                                                                                                                                                                                                                                      tuberculosis
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 78
                frequently
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 A; 139
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                                                                                                                                                               Heym
                                                                                                                                                                                              COUNCIL
                                                                                                                                                                                                                                                                                                                                                            gene fragment.
                                                                                                                                                                                                                                                                                                                                                                            entry)
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                by Leu.
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148
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Pred.
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67
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other.
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                                                                                                     tuberculosis
                                     The corresp.
                                              revealed
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                   Query Match
Best Local S
Matches 20
                                                                                                    (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 165/rrs
(streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
(ciprofloxacin) and 23s (azithromycin) genes of M. tuberculosis.
Characterization of M. tuberculosis present in a sputum sample.
The method involves performing a sequencing procedure, with or
without prior amplification, to detect the presence of M.
tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
Cand 23s genes for the presence of antibiotic-inducing mutations.
Claid 23s genes for the presence of antibiotic-inducing moutations.
Claid 23s genes for the presence of antibiotic-inducing moutations.
Claid 23s genes for the presence of antibiotic-inducing moutations.
Claid 23s genes for the presence of antibiotic-inducing procedure is performed on the sample to evaluate additional genes for the presence of antibiotic resistance-inducing mutations. Genotypic tests are rapid, sensitive and accurate providing information as to
                                                                                                                                                                                                                                      The present sequence is that of the Mycobacterium tuberculosis rpoB (rifampin resistance) gene (bp2161-2640). Amplification and cycle sequencing primers (see AAA49823-62) are used for the detect and analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PF (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs
                                                                                                                                                                                                                                                                                                                   Disclosure; Page 5; 43pp; English.
                                                                                                                                                                                                                                                                                                                                        Method for the detection and characterization of Mycobacterium tuberculosis with antibiotic resistance in a sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  primer_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA49863 standard;
                                                                         Sequence 480 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA49863;
                    / Match 100.0%;
Local Similarity 100.0%;
nes 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
tacggtcggcgagctgatcc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     resistance; rpoB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-CA01177
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                                                                                                                                                                                                                                                                                                                                                                                                                   GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers complement(41..60)
                                                                         89 A; 153 C;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpoB gene (rifampin resistance)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ВP
                                                                          163
                             Score 20; DB 21
Pred. No. 0.025;
                     Mismatches
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                                         21;
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                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        disease diagnosis; oligonucleotide; DNA primer;
ain reaction; DNA amplification; rpoB locus; TB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /*tag= b
/note= "primer
226..240
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/note= "M.
525..541
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/note=' "M.
468..469
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/note= "M.
433..434
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525
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516..535
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/note=
516
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501
      /*tag= q
/note= "primer rpo293"
640..666
                                       /*tag= p
/note= "primer KY292"
536..562
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438
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372..373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note- "primer DDIDH"
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                                                                                                                  "primer rpo273"
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nucleotide"

nucleotide"

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                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 20
                                                                               Mycobacterium
                                                                                                 Drug target; growth; organism viability; characterisation; ds
                                                                                                                         Mycobacterium tuberculosis potential drug target gene
                                                                                                                                                                                                                                                                                                                                                                                      tuberculosis, and may be used to amplify a sample DNA by targeting a portion of the gene encoding rpoB. The 1st several bases comprise nonhybridizing tail consisting of filler bases followed by a restriction site incorporated to facilitate cloning using the amplicon at a later date, if desired. The remaining bases hybridize to bacterial rpoB DNA. The method provides for the detection of M. susceptibility, particularly to rifamycin. The method can provide often greater than 95% sensitivity and 100% specificity. The biological sample is a fluid or tissue sample from a human.
                                  17-MAY-2001
                                                                                                                                                        04-SEP-2001
                                                                                                                                                                                                  AAH51976 standard; DNA; 3519 BP
          13-NOV-2000; 2000WO-US31152.
                                                          WO200135317-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This oligonucleotide DNA primer is specific for Mycobacterium tuberculosis, and may be used to amplify a sample DNA by targeting a portion of the gene encoding rpoB. The 1st several bases comprise a
                                                                                                                                                                                                                                                                                                                                                                     Sequence 970 BP; 182 A; 302 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Detection of Mycobacterium tuberculosis - by amplifying sample DNA with a primer set that targets portions of the gene encoding rpoB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig.3; 54pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1996-030581/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Felmlee TA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-MAY-1995;
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                                                                                                                                                                                                                                                                 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Young
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (HOFF ) HOFFMANN LA ROCHE INC. (MAYO-) MAYO FOUNDATION.
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20; Conserv
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ilarity 100.0%;
Conservative (
                                                                                                                                                    (first entry)
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                                                                               tuberculosis
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952..966
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/note= "primer NMQRQ-1"
952..966
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                                                                                                                                                                                                                                                               280
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                                                                                                                                                                                                                                                                                                                     Score 20; DB 17;
Pred. No. 0.023;
                                                                                                                                                                                                                                                                                                                                                                    330 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DH,
                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roberts GD,
                                                                                                                                                                                                                                                                                                                                                                   156 T; 0 other;
                                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                               Length 970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Whelen
                                                                                                                         SEQ ID
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                                                                                                                                                                                                                                                                                                       0;
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                                                                                                                                                                                                                                                                                                        Gaps
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Search completed: August Job time: 7610 sec
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                                                                                                  QΥ
                                                                                                                              Query Match
Best Local S
Matches 20
                                                                        1119
                                                                                                                                                                                                                                   method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1999;
12-NOV-1999;
01-FEB-2000;
                                                                                                                                                                                                                                                                                                                         This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polypucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The
                                                                                                                                                                                                    Sequence 3519 BP;
                                                                                                                                                                                                                                 an organism
                                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV
                                                                                 1 tacggtcggcgagctgatcc
                                                                  tacggtcggcgagctgatcc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2001-329193/34.
DB; AAG81125.
                                                                                                                          Similarity 100.
20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0165086.
99US-0165124.
2000US-0179531.
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Pred. No.
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                                                                                                                                        DB 22
0.021;
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Title:
Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Issued_Patents_NA:*
1: /cgn2_6/ptodata/2,
2: /ggn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/backfiles1.seq:*
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                                                                    US-08-313-185-59
US-08-757-653-136
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US-08-757-053-140
US-08-757-030-1
US-08-750-030-9
US-08-750-030-9
US-08-250-030-9
US-08-250-030-9
US-08-250-030-9
US-08-250-030-9
US-08-250-030-9
US-08-313-185-57
US-08-906-616-169
US-08-906-613-169
US-08-906-613-169
US-08-906-613-119
US-08-906-613-171
US-08-906-613-171
US-08-906-758-171
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Compugen Ltd
                                               Sequence 59, Appl
Sequence 135, App
Sequence 136, App
Sequence 137, App
Sequence 138, App
Sequence 139, App
Sequence 140, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 169, Appl
Sequence 169, App
Sequence 171, App
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US-08-998-416-615	US-08-282-696-20	US-08-459-586-20	PCT-US96-04648-4	US-08-282-696-19	US-08-459-586-19	US-08-976-259-123	US-08-636-928-6	US-09-103-840A-2	US-09-232-201-64	US-09-232-197-64	US-09-232-200-64	US-09-360-682A-1	US-08-896-344A-1	US-09-232-201-29	US-09-232-197-29	US-09-232-200-29	us-08-906-613-171
Sequence 615, App	Sequence 20, Appl	Sequence 20, Appl	Sequence 4, Appli	Sequence 19, Appl	Sequence 19, Appl	Sequence 123, App	Sequence 6, Appli	Sequence 2, Appli	Sequence 64, Appl	Sequence 64, Appl	Sequence 64, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 29, Appl	Sequence 29, Appl	Sequence 29, Appl	Sequence 171, App

ALIGNMENTS

RESULT

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TOPOLOGY: 1:

MOLECULE TYPE:
US-08-313-185-59
                                                          REFERENCE DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4000
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: Single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-313-185-59/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; Patent No. 5851763
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                 COUNTRY: USA

CIP: 20005-3315

CIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/313,185

FILING DATE: 12-OCT-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

DEFERENCE OF THE MEYERS AT TOWNEY NUMBER: 25,146

DEFERENCE OF THE MEYERS AT TOWNEY NUMBER: 25,146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Endine, Amalio
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Finnegan, Henderson,
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59,
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5851763
                                                     linear
                       DNA (genomic)
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US-08-757-653-135/c; Sequence 135, Appl; Patent No. 5843669
                                               RESULT
                                                                                                                                                                                                                                ; STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) US-09-082-614A-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-082-614A-59/c
                                                                                                                                                           Matches
                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                         TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 100 Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994
ATTORNEY/ACENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Voung, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
                                                                                        428 TACGGCGTTTCGATGAACCC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
                                                                                                                                                   Local Similarity 100.
nes 20; Conservative
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CITY: Washington
STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 02:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/082,614A FILING DATE: CLASSIFICATION:
                                                                                                            1 tacggcgtttcgatgaaccc 20
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Meyers, Kenneth REGISTRATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    428 TACGGCGTTTCGATGAACCC 409
                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 tacggcgtttcgatgaaccc 20
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                                                                                                                                                                                                                                                                                      nucleic acid
             Application US/08757653
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Pred. No.
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); Mismatches 0;
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                                                                                                                                                                             Length 432;
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                                                                              ZIP:
                                                                                             COUNTRY:
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US-08-757-653-136/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: FOR:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 136, Application US/08757653 Patent No. 5843669
                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                     APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296 TACGGCGTTTCGATGAACCC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                                                                                     ADDRESSEE: Medlen & Carluit, Suite 2200 STREET: 220 Montgomery Street, Suite 2200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 tacggcgtttcgatgaaccc 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 220 FCCCITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94104
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                                                                                                                                             United States Of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435

US/08/757,653

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US-08-757-653-137/c
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INFORMATION FOR SEQ ID NO: 13
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 137, Application US/08757653 Patent No. 5843669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                              TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                              REFERENCE/DOCKET NUMBER: FOI TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                    FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Kaiser, Michael W. APPLICANT: Lyamichev, Victor I. APPLICANT: Lyamichev, Natasha
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NAME: Ingolia, Diane E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Cleavage Of Nucleic Acid Using TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 40,
                                                                                                                                                                                 NAME: Ingolia, Diane REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
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                               STRANDEDNESS:
                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
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                                                                    ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                           94104
                                             nucleic acid
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                     linear
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 DNA (genomic)
                                   double
                                                                                                                                                                                                                                                                       US/08/757,653
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Pred. No. 0.00054;
); Mismatches 0;
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; MOLECULE TYPE:
US-08-757-653-138
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Patent No.
                                                                                                                                                                                                                                 Sequence 139, Application US/08757653 Patent No. 5843669
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Best Local Similarity
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Best Local Similarity
                            GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kaiser, Michael W. APPLICANT: Lyamichev, Victor I. APPLICANT: Lyamichev, Natasha TITLE OF INVENTION: Cleavage Of TITLE OF INVENTION: Thermostabl NUMBER OF SEQUENCES: 190 CORRESPONDENCE ADDRESS:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
CONTROL CO
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ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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MEDIUM TYPE: Floppy disk
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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STREET: 220 Montgomery Street,
CITY: San Francisco
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Lyamichev, Natasha
NVENTION: Cleavage Of Nucleic Acid Using
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Thermostable FEN-1
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Pred. No. 0.00054; __
Pred. No. 0.00054; __
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REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 139:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No. 5843669
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 140, Application US/08757653 Patent No. 5843669
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            CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,
                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                  APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-I Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Kaiser, Michael W. APPLICANT: Lyamichev, Victor I. APPLICANT: Lyamichev, Natasha
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                                                                                                                                                                                                                                                                   STREET: 220 MONTGOME CITY: San Francisco
REFERENCE/DOCKET NUMBER:
                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                        ADDRESSEE: Mequen Street,
                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                              STATE:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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STREET: 220 Montgomery Street, Suite 2200
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                  40,027
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FORS-02565
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                                                                                                                                                                                                                                                                                          Suite 2200
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US-08-797-812-24/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local :
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 397-8338 INFORMATION FOR SEQ ID NO:
           TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 35,
                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,765
FILING DATE: 15-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/629,031
FILING DATE: 08-ARR-1996
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APPLICANT:
APPLICANT:
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APPLICATION NUMBER: US 60/011,339
FILING DATE: 08-FEB-1996
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: TWO CITY: San Francisco
STATE: CA
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Chip-Based Species Identification and TITLE OF INVENTION: Phenotypic Characterization of Microorganisms ONLY SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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REFERENCE/DOCKET NUMBER: 16
                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 07-FEE CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE:
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Wang, Ching
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                                                                                                                                                                                                                                                                                                                                                             PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Berno, Anthony J.
Stryer, Lubert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mack, David
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Chee, Mark S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gingeras,
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                                                                                                                                                                 UMBER: US 60/012,631
01-MAR-1996
                                                                                                                                                                                                                                                                                                                    UMBER: US/08/797,812
07-FEB-1997
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GENERAL INFORMATION:

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RESULT 11
PCT-US95-06790-1/c
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US-08-250-030-1
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                                                                                                                                   Best Loc
Matches
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                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                         TELEFAX: 612-339-3061 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: Patchtin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,030
FILING DATE: 26-MAY-1994
                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 612-339-0331
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                            671 TACGGCGTTTCGATGAACCC 652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 332 TACGGCGTTTCGATGAACCC 313
                                                                                                                                                                                                                                                LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                              NAME: Mueting, Ann M. REGISTRATION NUMBER: 33,977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UZIP: 55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET:
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                                                                                                                                   Local Similarity 100. 
les 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                           1 tacggcgtttcgatgaaccc 20
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3500 IDS Center
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100.0%; F
1tive 0;
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Clinical Specimens
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                                                                                                                                  Score 20; DB
Pred. No. 0.0
0; Mismatches
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Pred. No. 0.00053;
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                                                                                                                                                 0.00053;
                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Locus Encoding in Mycobacterial Cultures
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                                                                                                                                                             Length 970;
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                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 71,
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Best Local :
                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                         APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
APPLICATION NUMBER: PCT/US95/06790
                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                             TITLE OF INVENTION: ME
TITLE OF INVENTION: RE
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           671 TACGGCGTTTCGATGAACCC 652
                                                                                        COUNTRY:
ZIP: 200
                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                           ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C STREET: 1100 NEW YORK AVENUE, SUITE 600 CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Raasch, Kevin W. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                            STATE: D.C
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ROSSAU,
                                                                                                                                                                                                                                                                                                          DE BEENHOUWER, HANS PORTAELS, FRAN OISE MACHTELINCKX, LIEVE
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PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                    METHOD FOR DETECTION OF THE ANTIBIOTIC RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES: 71
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US-08-250-030-9
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US-08-250-030-9
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Best Local :
                                                                                                        TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
              MOLECULE TYPE:
                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                   REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 15
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
                                                                                                                                                                                                                 APPLICATION NUMBER: US/00
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Persing, TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 167
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                             TOPOLOGY:
                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       / Match 95.0%; Sc Local Similarity 100.0%; P Conservative 0;
                                                                          LENGTH:
                                                                                                                                                                                                         NAME:
                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 21-FEI CLASSIFICATION:
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                                       H: 27 base pairs
nucleic acid
DEDNESS: single
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Mueting, Ann M.
MITMBER: 33,977
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29,021
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Resistance to Rifampin in Mycobacterial Cultures and
Clinical Specimens
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RESULT 15
US-08-313-185-57/c
                                                                                  ; Patent No. 3851763
; GENERAL INFORMATION:
; APPLICANT: Heym, Ba
; APPLICANT: Cole, S:
; APPLICANT: Young, I
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PCT-US95-06790-9
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Best Local Similarity
Matches 15; Conserva
                                                                                                                                              Sequence 57, Application US/08313185
Patent No. 5851763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application PC/TUS9506790 GENERAL INFORMATION:
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Best Local
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REFERENCE/DOCKET NUMBER: 150.
TELECOMMUNICATION INFORMATION:
TELECHONE: 612-339-0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO:
                                                         APPLICANT:
APPLICANT:
           APPLICANT:
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LENGTH: 27 base pairs
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MEDIUM TYPE: Floppy
                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Mayo Foundation for Medical Education and Research APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
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TOPOLOGY: linear
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 55402
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T: Young, Douglas
T: Zhang, Ying
T: Honore, Nadine
T: Telenti, Amalio
T: Bodmer, Thomas
T: Bodmer, Rapid Detection of Antibiotic Resistance
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Cole, Stewart
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NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Ptetentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: USA/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION NUMBER: USA/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION NUMBER: 25,146
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-313-185-57
                                                                                                                        밁
Search completed: August 7, 2002, 23:51:48 Job time: 7174 sec
                                                                                                                                                                                                                  Ouery Match 70.0%; Score 14; DB 2; Length 3447; Best Local Similarity 100.0%; Pred. No. 2.7; Matches 14; Conservative 0; Mismatches 0; Indels
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1448 GTTTCGATGAACCC 1435
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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// SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1999.DAT:*

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// SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*

// SIDS1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*

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Gapop 10.0 , Gapext 1.0
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Copyright (c) 1993 - 2000 Compugen Ltd
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
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/SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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DB
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               AAT12092
AAA49825
AAA49825
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RpoB gene fragment
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	AAS99565	AAS99560		AAS99534	AAX27189	AAX27186	AAX27204	AAX27198	AAX27220	AAX27219	AAX27216	AAX27212	AAC88922	AAS59541	AAS99557	AAS99539	AAX27183	AAX27182	AAX27177	AAX27196	AAX27193	AAX27218	AAT12091	AAS59633	AAS99551	AAX27217	AAA89994	AAA74651	20	AAH51976	96	86	14	953	AAS99530	
	Mycobacterium spec			bacteri	gene	gene f	gene f	gene f	gene	gene	gene	RpoB gene fragment	Mycobacterium tube	Propionibacterium		bacter	gene	gene	gene	gene	gene	ъВ gene fragmen	M. tuberculosis rp	Propionibacterium	Mycobacterium spec	oB gene fragmen		Mycobacterium tube				_	M.tuberculosis rpo	as	Mycobacterium spec	

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ALIGNMENTS

RESULT Antibiotic; resistance; spectrum; gene; mycobacterium; determination; amplification; tuberculosis; rpoB; fragmen primer; differential; hybridisation; pattern; rifampicin; rifabutin; species identification; ss. 09-JUN-1994; Synthetic M. tuberculosis rpoB gene fragment amplification primer P2. 10-JUL-1996 AAT12092; AAT12092 standard; DNA; 20 BP (INNO-) INNOGENETICS NV. 09-JUN-1995; 14-DEC-1995 (first entry) 94EP-0870093 95WO-EP02230

RpoB gene fragment RpoB gene fragment RpoB gene fragment RpoB gene fragment

Mycobacterium Mycobacterium

WPI; 1996-040250/04

Rossau R; De Beenhouwer H,

> Jannes 9

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RESULT
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     rpoB (rifampin resistance) gene amplification primer rpoB-F (bp 2201-2220). It is used with the reverse primer given in AAA49824 and with the sequencing primers given in AAA49825 and AAA49826 for the detection and analysis of antibiotic resistance-associated mutations of the rpoB gene (see AAA4983). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and analysis of antibiotic resistance-associated mutations in defined
  regions of rpoB (rifampin),
                                                                                                      The present sequence is that of the Mycobacterium tuberculosis
                                                                                                                                     Claim 4; Page 4; 43pp; English.
                                                                                                                                                          Method for the detection and characterization of Myctuberculosis with antibiotic resistance in a sample
                                                                                                                                                                                                                                                                                         11-DEC-1998;
                                                                                                                                                                                                                                                                                                                   10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The antibiotic resistance spectrum (ARS) of a mycobacterium can be determined by amplifying the relevant part of the antibiotic resistance gene, i.e. the M. tuberculosis rpoB gene fragment amplified using the primer set ART12091-98, hybridising it with a least 1 rpoB gene probe, detecting the hybrids formed and inferring the ARS, and opt. the spp., from the differential hybridisation patterns. The method is partic. useful for the detection of rifampicin and/or rifabutin resistance in M. leprae or M. tuberculosis, and mycobacterial spp. identification. The method is rapid and reliable and provides simultaneous determn.
                                                                                                                                                                                                                                                              (VISI-) VISIBLE GENETICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA49823 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Probes and primers for determn. of antibiotic resistance spectrum of Mycobacterium, opt. coupled with species identification – from different patterns of hybridisation with rpoB gene
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RESULT
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Best Local
The present sequence is that of the Mycobacterium tuberculosis rpoB (rifampin resistance) gene sequencing primer rpoB-5s (bp 2201-2220). It is used with the reverse primer given in AAA49826 and with the amplification primers given in AAA49823 and AAA49824 for the detection and analysis of antibiotic resistance-associated mutations of the rpoB gene (see AAA49863). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR (isoniazid), mabA (isoniazid), rpoA (pyrazinamide), gyrA (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
                                                                                                                                                                                                         Claim 4; Page 5; 43pp; English.
                                                                                                                                                                                                                                     Method for the detection and characterizati
                                                                                                                                                                                                                                                                                      WPI; 2000-431611/37.
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Pred. No. 1
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                         This sequence represents a mycobacterial rpoB gene fragment, that is amplified using the PCR primers of the invention. The primers form a method of detecting and identifying mycobacterial species by constructing a phylogenetic tree for the species. The use of the primers for sequence-specific amplification of the rpoB gene (encoding the beta subunit of RNA polymerase) from mycobacterial species provides an efficient way of characterising these species. In addition to phylogenetic analysis, the rpoB gene can be used as an alternative to the 16s rRNA gene because it has four subunits, which are highly conserved throughout prokaryotes. The method is particularly useful for slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              These primers can be used in a method for the detection and characterization of M. tuberculosis present in a sputum sample. The method involves performing a sequencing procedure, with or without prior amplification, to detect the presence of M. tuberculosis, and if present to evaluate the rpoB, katG, rpsL/sl2 and 23S genes for the presence of antibiotic-inducing mutations. If M. tuberculosis is detected, a second sequencing procedure is performed on the sample to evaluate additional genes for the presence of antibiotic resistance-inducing mutations. Genotypic tests are rapid, sensitive and accurate providing information as the sample to evaluate additional sensitive and accurate providing information as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    кров gene; mycobacteria; mycobacterial species ide
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slow growing, fasti
susceptibility can
                                                                                                                                                                                                                                                                                                                                                                                                          Claim 43; Page 75-76;
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identification; phylogenetic analysis;
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                                                                                                                                      susceptibility can be simultaneously determined in M. tuberculosis.
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                                                                                                               G; 47 T;
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Best Local
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                           RpoB gene; mycobacteria; phylogenetic tree construction; mycobacterial species identification; phylogenetic analysis;
          Mycobacteria bovis
                                                                        RpoB gene
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                                                                                                                                                                                                                                                                                                                                                                                                                             Drug resistance oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium species identification primer
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                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis.
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rpoB; sputum; blood; cerebrospinal fluid; s
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                                                              Kit for mycobacterial species identification and drug resistance detection, has oligonucleotide chip with species identification a mycobacterial drug-resistance detection probe, and its contrast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identification and drug resistance detection comprising an oligonucleotide chip including a species identification probe, a mycobacterial drug-resistance detection probe, a contrast group
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chip; rpoB; sputum; blood; cerebrospinal fluid; ;
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Disclosure; Page

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The invention relates to a diagnostic kit for mycobacterial species identification and drug resistance detection comprising an oligonucleotide chip including a species identification probe, a mycobacterial drug-resistance detection probe, a contrast group prob corresponding to each drug resistance detection probe, and a marker detecting a hybridisation of the oligonucleotide chip and a specimen identification probe is comprised of species-specific DNA sequences

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a diagnostic kit for mycobacterial species identification and drug resistance detection comprising an oligonucleotide chip including a species identification probe, a
                                                                                                                               Kit for mycobacterial species identification and detection, has oligonucleotide chip with species a mycobacterial drug-resistance detection probe,
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                                                                                                                                                                                                        Kim H,
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            mycobacterial rpoB gene and the detection probe is comprised of one or more modified codons of mycobacterial rpoB gene and the detection probe is comprised of one or more modified codons of mycobacterial rpoB gene. The method involves amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction (PCR) and discriminating species by fluorescent intensity corresponding to a particular species. The specimen is preferably uncultured sputum, blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569 represent mycobacterium appears in the specimen is sequences.
                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 21; 74pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Kit for mycobacterial species identification and drug resistance detection, has oligonucleotide chip with species identification a mycobacterial drug-resistance detection probe, and its contras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drug resistance detection; mycobacterial species identification; probe; oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ss;
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                     PCR amplification was used to obtain rpoB genes from rifamplcin-resistant Mycobacterium leprae strains. A comparison with the sequence of the rpoB gene from sensitive strains (AAQ51532) revermutations in the region encoding amino acids 400-450. The correspression was isolated from M.tuberculosis (AAQ61457). A common mutation seen in resistant strains occurs at codon 425 where Ser
                  mutation seem
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                                                                                      Fig 13; 97pp; English.
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                                                                                                                                                                                                                                                                                                                                                                     antibiotic; susceptibility; sensitive; resistant; rpoB;
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92US-0875940.
92US-0929206.
93FR-0004545.
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78 A; 139
                frequently by Leu.
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AAA49863
                                                                                                                                The present sequence is that of the Mycobacterium tuberculosis CC rpoB (rifampin resistance) gene (bp2161-2640). Amplification and CC cycle sequencing primers (see AAA49823-62) are used for the detection CC and analysis of antibiotic resistance-associated mutations in CC (isoniazid), mabA (isoniazid), resistance-associated mutations in CC (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 165/rrs CC (streptomycin), embB (ethamburol), pncA (pyrazinamide), gyrA CC (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis. CC These primers can be used in a method for the detection and CC characterization of M. tuberculosis present in a sputum sample. CC The method involves performing a sequencing procedure, with or CC without prior amplification, to detect the presence of M. tuberculosis, and if present to evaluate the prob, katG, rpsL/s12 CC and 23S genes for the presence of antibiotic-inducing mutations. CC performed on the sample to evaluate additional genes for the presence of antibiotic resistance-inducing mutations. Genotypic CC tests are rapid, sensitive and accurate providing information as to CC cantibiotic treatment options.
                                           Query Match
Best Local S
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                                                                                                          Sequence 480
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                                                                                                          BP; 89 A; 153 C;
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ain reaction; DNA amplification; rpoB locus; TB;
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Best Local Similarity
Matches 20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This oligonucleotide DNA primer is specific for Mycobacterium tuberculosis, and may be used to amplify a sample DNA by targeting a portion of the gene encoding rpoB. The 1st several bases comprise nonhybridizing tail consisting of filler bases followed by a restriction site incorporated to facilitate cloning using the amplicon at a later date, if desired. The remaining bases hybridize to bacterial rpoB DNA. The method provides for the detection of M. tuberculosis and the concurrent determination of its drug susceptibility, particularly to rifamycin. The method can provide often greater than 95% sensitivity and 100% specificity. The biological sample is a fluid or tissue sample from a human.
                                                                                                                                                                      Mycobacterium
                          13-NOV-2000; 2000WO-US31152
                                                                           17-MAY-2001
                                                                                                                             WO200135317-A1
                                                                                                                                                                                                                   Drug target; growth; organism viability; characterisation; ds
                                                                                                                                                                                                                                                                          Mycobacterium
                                                                                                                                                                                                                                                                                                                         04-SEP-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detection of Mycobacterium tuberculosis - by amplifying sample DNA with a primer set that targets portions of the gene encoding rpoB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 970 BP; 182 A; 302 C;
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                                                                                                                                          This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polypucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of an analysis.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Mycobacterium spec	Mycobacterium spec	RpoB gene fragment	RpoB gene fragment	RpoB gene fragment	RpoB gene fragment	Mycobacterium tube	Mycobacterium tube	M. tuberculosis rp	Description	

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Mycobacterium spec Mycobacterium spec	-	Mycobacterium spec	pacter	gene	RpoB gene fragment	Mycobacterium tube	Propionibacterium		pacter	gene	gene	gene	gene	gene	рв gene	M. tuberculosis rp	Propionibacterium	Mycobacterium spec	RpoB gene fragment	M. tuberculosis rp	Mycobacterium tube		spe	Mycobacterium spec										

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ALIGNMENTS

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RESULT 1
AAT12092
ID AAT12092 standard; DNA;
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20 BP.

10-JUL-1996 (first entry)

M. tuberculosis rpoB gene fragment amplification primer P2

Antibiotic; resistance; spectrum; gene; mycobacterium; determination; amplification; tuberculosis; rpoB; fragment; primer; differential; hybridisation; pattern; rifampicin; rifabutin; species identification; ss.

Synthetic



09-JUN-1994; 94EP-0870093

98-2000-1995

9500-EP0225

(INNO-) INNOGENETICS NV.

Rossau R; De Beenhouwer H, Jannes ç, Machtelinckx L, Portaels Ħ

WPI; 1996-040250/04

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RESULT
ANA49823
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Best Local :
          rpoB (rifampin resistance) gene amplification primer rpoB-F (bp 2201-2220). It is used with the reverse primer given in AAA49824 and with the sequencing primers given in AAA49825 and AAA49826 for the detection and analysis of antibiotic resistance-associated mutations of the rpoB gene (see AAA49863). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and analysis of antibiotic resistance-associated mutations in defined
                                                                                                             The present sequence is that of the Mycobacterium tuberculosis rpoB (rifampin resistance) gene amplification primer rpoB-F (b)
       regions of rpoB (rifampin),
                                                                                                                                                                      Claim 4; Page 4; 43pp; English.
                                                                                                                                                                                                Method for the detection and characterization of Mycobacterium tuberculosis with antibiotic resistance in a sample \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                              Shipman R;
                                                                                                                                                                                                                                                                                                                           (VISI-) VISIBLE GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200036142-A1
                                                                                                                                                                                                                                                                                                                                                                                              10-DEC-1999;
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                                                                                                                                       The present sequence is that of the Mycobacterium tuberculosis rpoB (rifampin resistance) gene sequencing primer rpoB-5s (bp 2201-2220). It is used with the reverse primer given in AAA49826 and with the amplification primers given in AAA49823 and AAA49824 for the detection and analysis of antibiotic resistance-associated mutations of the rpoB gene (see AAA49863). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and
analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rrs (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 5; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                          Method for the detection and characterization of Mycobacterium tuberculosis with antibiotic resistance in a sample - \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2000-431611/37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              These primers can be used in a method for the detection and characterization of M. tuberculosis present in a sputum sample. The method involves performing a sequencing procedure, with or without prior amplification, to detect the presence of M. tuberculosis, and if present to evaluate the rposh, katc, rpsL/sl2 and 23S genes for the presence of antibiotic-inducing mutations. If M. tuberculosis is detected, a second sequencing procedure is performed on the sample to evaluate additional genes for the presence of antibiotic resistance-inducing mutations. Genotypic tests are rapid, sensitive and accurate providing information as the contract of the presence of antibiotic resistance-inducing mutations.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (VISI-) VISIBLE GENETICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5s.
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Length 306;

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This sequence represents a mycobacterial rpoB gene fragment, that is amplified using the PCR primers of the invention. The primers form a method of detecting and identifying mycobacterial species by constructing a phylogenetic tree for the species. The use of the primers for sequence-specific amplification of the rpoB gene (encoding the beta subunit of RNA polymerase) from mycobacterial species provides an efficient way of characterising these species. In addition to phylogenetic analysis, the rpoB gene can be used as an alternative to the 16S TRNA gene because it has four subunits, which are highly conserved throughout prokaryotes. The method is particularly useful for slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin susceptibility can be simultaneously determined in M. tuberculosis.
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subunit of RNA polymerase) from mycobacterial species provides an
efficient way of characterising these species. In addition to
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                                                                                                                                        susceptibility can be simultaneously determined in M. tuberculosis.
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                                                               Score 20; DB Pred. No. 1.6;
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Best Local
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                                        RpoB gene; mycobacteria; mycobacterial species id:
               Mycobactería bovis
                                                                               RpoB gene
                                                                                                             27-MAY-1999
                                                                                                                                                              AAX27180 standard; DNA; 306 BP
                                                                                                                                                                                                                                                                                                                                                        Sequence
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                                  .a; phylogenetic tree construction; identification; phylogenetic analysis; ss.
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Best Local (
          Kim H,
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                                                          30-MAY-2000; 2000KR-0029369
                                                                                                              06-DEC-2001.
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                                                                                                                                                                                                  Drug resistance oligonucleotide
                                                                                    30-MAY-2001; 2001WO-KR00904
                                                                                                                                                             Mycobacterium tuberculosis
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        Yoon S,
                                                                                                                                                                                                 detection; mycobacterial species identification;
chip; rpoB; sputum; blood; cerebrospinal fluid;;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kit for mycobacterial species identification and detection, has oligonucleotide chip with species a mycobacterial drug-resistance detection probe,
                                                                                                                                                                                                                                                                                                        Drug resistance detection; oligonucleotide chip; rpoB;
 Disclosure;
                                   Kit for mycobacterial species identification and drug resistance detection, has oligonucleotide chip with species identification probe, and its contras.
                                                                                                                                                                30-MAY-2000; 2000KR-0029369
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                                                                                                                                                                                                                                                                                                        mycobacterial species identification; probe;
; sputum; blood; cerebrospinal fluid; ss;
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The invention relates to a diagnostic kit for mycobacterial species identification and drug resistance detection comprising an oligonucleotide chip including a species identification probe, a mycobacterial drug-resistance detection probe, a contrast group prob corresponding to each drug resistance detection probe, and a marker detecting a hybridisation of the oligonucleotide chip and a specimen

a specimen. The sequences of

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                                                                                               Disclosure;
                                                                                                                              Kit for mycobacterial species identification and drug resistance detection, has oligonucleotide chip with species identification probe, a mycobacterial drug-resistance detection probe, and its contrast group
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chip; rpoB;
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                 identification and drug resistance detection comprising an oligonucleotide chip including a species identification probe, a mycobacterial drug-resistance detection probe, a contrast group probe corresponding to each drug resistance detection probe, and a marker for detecting a hybridisation of the oligonucleotide chip and a specimen. The identification probe is comprised of species-specific DNA sequences of mycobacterial rpoB gene and the detection probe is comprised of one or more modified codons of mycobacterial rpoB gene. The method involves amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction (PCR) and discriminating species by fluorescent intensity corresponding to a particular species. The specimen is preferably uncultured sputum, blood or cerebrospinal fluid of a patient. Sequences AAS9978-AAS99569
    represent mycobacterium
                                                                                                                                                                                                                                                                                                           The invention relates to a diagnostic kit for mycobacterial
                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kit for mycobacterial species identification and drug resistance detection, has oligonucleotide chip with species identification |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drug resistance detection; mycobacterial species identification; oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   more modified codons of mycobacterial rpoB gene. The method involves amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction (PCR) and discriminating species by fluorescent intensity corresponding to a particular species. The specimen is preferably uncultured sputum, blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569 represent mycobacterium species identification probes and primers of the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BIOM-) BIOMEDLAB CO LTD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium species identification primer #6.
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llarity 100.0%;
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species identification probes and primers of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             306
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                                                                                                                                                                                                                                                                                                                                                             English
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                                                                                                                                                                                                                                                                                                                                                                                                                               identification probe, and its contrast grou
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Query Match Best Local Matches 2

Similarity

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Best Local
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30-APR-1992;
14-AUG-1992;
16-APR-1993;
                      PCR amplification was used to obtain rpoB genes from rifampicin-resistant Mycobacterium leprae strains. A comparison with the sequence of the rpoB gene from sensitive strains (AAQ51532) revermutations in the region encoding amino acids 400-450. The correspregion was isolated from M.tuberculosis (AAQ61457). A common mutation seen in resistant strains occurs at codon 425 where Ser
                                                                                                    Rapid detection of antibiotic resistance in Mycobacteria - esp. isoniazid, rifampicin or streptomycin resistance in tuberculosis by detecting mutation in katG, rpoB or rpsL genes
Sequence
                  substituted,
                                                                                      Example
                                                                                                                                                   WPI;
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                                                                                                                                                                                           (UYPA-)
                                                                                                                                                                                                    (MEDI-)
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                                                                                                                                                                                                                                                                                                                                           Mycobacterium
                                                                                                                                                                                                                                                                                                                                                             mutant;
                                                                                                                                                                                                                                                                                                                                                                   rifampicin;
                                                                                                                                                                                                                                                                                                                                                                                   M.tuberculosis rpoB gene fragment
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ВP;
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                                                                                                                                                                                                                                                                                                                                           tuberculosis
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92US-0875940.
92US-0929206.
93FR-0004545.
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148 G;
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                                                                                                                 The present sequence is that of the Mycobacterium tuberculosis crops (rifampin resistance) gene (bp2161-2640). Amplification and cycle sequencing primers (see AAA48823-62) are used for the detection and analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 165/rrs (streptomycin), embB (ethambutch), pncA (pyrazhamide), syrA (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis. These primers can be used in a method for the detection and characterization of M. tuberculosis present in a sputum sample. The method involves performing a sequencing procedure, with or without prior amplification, to detect the presence of M. tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12 and 23S genes for the presence of antibiotic-inducing mutations. If M. tuberculosis is detected, a second sequencing procedure is
                                                                                          performed on the sample to evaluate additional genes for the presence of antibiotic resistance-inducing mutations. Genoty tests are rapid, sensitive and accurate providing information
                                                                                                                                                                                                                                                                         Disclosure; Page 5; 43pp; English.
                                                                                                                                                                                                                                                                                          primer_bind
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                                                               Sequence 480 BP; 89 A; 153 C; 163
                                                                                                                                                                                                                                                                                                                       WPI; 2000-431611/37.
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                                                                                                                                                                                                                                                                                                                                                                                                10-DEC-1999;
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1 tacggtcggcgagctgatcc 20
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                                                                                 treatment options.
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llarity 100.0%;
Conservative (
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372..391
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                  0;
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Pred.
                 Mismatches
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                           1.6;
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354..373
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226..240
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226..243
        /note- "primer rpo293" 640..666
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Matches 20
           13-NOV-2000; 2000WO-US31152
                                                                                Mycobacterium tuberculosis
                                                                                                   Drug target; growth; organism viability; characterisation; ds
                                                                                                                          Mycobacterium tuberculosis potential drug target gene
                                                                                                                                                      04-SEP-2001
                                                                                                                                                                                                  AAH51976 standard; DNA; 3519 BP
                                                                                                                                                                                                                                                                                                                                                                                       to bacterial rpoB DNA. The method provides for the detection of M tuberculosis and the concurrent determination of its drug susceptibility, particularly to rifamycin. The method can provide often greater than 95% sensitivity and 100% specificity. The biological sample is a fluid or tissue sample from a human.
                                                                                                                                                                                                                                                                                                                                                                                                                                    This oligonucleotide DNA primer is specific for Mycobacterium tuberculosis, and may be used to amplify a sample DNA by targeting a portion of the gene encoding rpoB. The 1st several bases comprise a nonhybridizing tail consisting of filler bases followed by a restriction site incorporated to facilitate cloning using the amplicon at a later date, if desired. The remaining bases hybridize to bacterial rpoB DNA. The method provides for the detection of M.
                                   17-MAY-2001
                                                          WO200135317-A1
                                                                                                                                                                                                                                                                                                                                                                     Sequence 970 BP; 182 A; 302 C;
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1119 tacggtcggcgagctgatcc

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                                                                                                                                          This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of an organism
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12-NOV-1999;
01-FEB-2000;
                                                                                                            Sequence 3519
                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 68-69;
                                                                                                                                                                                                                                                                                                                                                                    Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
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BASE COUNT ORIGIN RESULT 15 AE006964/c REFERENCE AUTHORS SOURCE ORGANISM REFERENCE AUTHORS 밁 ş KEYWORDS DEFINITION FEATURES VERSION ACCESSION rocus TITLE JOURNAL Ouery Match Best Local Matches TITLE JOURNAL 2611 TACGGCGTTTCGATGAACCC CDS gene source 1 tacggcgtttcgatgaaccc AE006964 Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E., Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H., Gill,J., Mikula,A. and Bishai,W.
Whole genome comparison of Mycobacterium tuberculosis clinical and laboratory strains Mycobacterium tuberculosis CDC1551.
Mycobacterium tuberculosis CDC1551
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex. AE006964 AE000516 AE006964.1 GI:13880217 Direct Submission
Submitted (25-APR-2001) The Institute f
Medical Center Dr. Rockville, MD 20850, Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,C peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E. Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H. Gill,J., Mikula,A. and Bishai,W. Mycobacterium tuberculosis CDC1551, Unpublished 2 (bases 1 Fleischmann, R.D., Alland, D., Eisen, J.A., Similarity (bases 1 to 19352) (bases 1 to 19352) Conservative ø /translation="MLDVNFFDELRIGLATAEDIRQWSYGEVKKPETINYRTLKPEKD GLFCEKLFGPTRDWECYCGKYRAVRFKGIICERCGVEVTRAKVRRERMGHIELAAPVT HIMYFKQVPSRLGYLLDLAPKDLEKIYFAAYVITSVDEEMRHNEL" a 1534 c 1691 g 890 t /gene=' /product-"DNA-directed RNA polymerase, beta subunit"
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/db_xref-"G1:13880218"
/translation-"MLEGCILADSROSKTAASPSPSRPOSSSNNSVPGAPNRVSFAKL
/translation-"MLEGCILADSROSKTAASPS /note="similar to GB:L27989 GB:L05910 GB:U12205 PID:149992; identified by sequence similarity; procession of the companies of 163. /organism="Mycobacterium /strain="CDC1551" /db_xref="taxon:83331" RDTVGVRIDRKRRQPVTVLLKALGWTSEQIVERFGFSEIMRSTLEKDNTVGTDEALLD IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT EEDVVATIEYLVRLHEGQTTMTVPGGVEVPVETDDIDHFGNRRLRTVGELIQNQIRVG MSRMERVVRERMTTQDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRMCPIETPEGPNIGLIGSLSVYARVNP Location/Qualifiers /transl_table=11 /codon_start=1 /gene="MT0695" /note="clinical 100.0%; . 3699 . 3699 'MT0695" 20 0; Score 20; Pred. No. 19352 bp strain" Mismatches 0.058; DB 1; tuberculosis CDC1551" DNA NA linear BCT 27-APR-2001 section 50 of 280 of the for Genomic), USA 0 Length 5084; Carpenter, L., White, O. M., Haft, D., Hickey, E., Research, 0, Khouri, H., White, O., White, O.,)5 SP:P47766 putative" Gaps 0;

> /gene="MT0696" 3744. .7694 /gene="MT0696" CANQCPTYDAGDRYEAGQVIADGPCTDDGEMALGKNILLVAIMPWEGHNYEDAIILSNR
> LVEEDYLTS.HIEEHEIDARDTKLGAEEITRDIPNISDEVLADLDERGIVRIGAEVRD
> GDILVGKYTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGESGKVIGIRVETSE
> DEBELEAGVNELLVRVYYAQKRKISDGDKLAGRRGNKGVIGKILPVEDMPFLADGTPVD
> IILNTHGVPRRMNIGOJLETHLGWCAHSGWKVDAAKGVPDWAARLPDELLEAAQNNAIV
> STPVFDGAQEAELOGLLSCTLPNRDGDVLVDADDKAMLFDDELGGEPFPVPTVGYMYI
> MKLHHLVDDKIHARSTGPYSMITQQPLGGKAQFGGQRRGEMECWAMQAYGAATTLQEL
> LTIKSDDTVGRVKYYEAIVKGENIPEFGIPESFKVLLKELQSLCLNVEVLSSDGAAIE FGFIETPYRKVVDGVVSDEIVYLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG EVEYVPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMQRQAVPLVRSEAP LVGTGMELRAAIDAGDVVVAEESGVIEEVSADVITVMHDNGTRRTYRMRKFARSNHGT FKHEDGSERVLSDGDHVEVGQQLMEGSADPHEVLRVQGPREVQHHVREVQEVYRAQG VSIHDKHIEVIVRQMLRRVTIIDSGSTEFLPGSLLDRAEFEAENRRVVAEGGEPAAGR PVLMGTTKASLATDSWLSAASFOETTRVLTDAAINCRSDKLNGLKENVIIGKLIPAGF GINRYRNIAVQPTEEARAAAYTIPSYEDQYYSPDFGAATGAAVPLDDYGYSDYR LREGEDEDLERAAANLGINLSRNESASVEDLA" 3744. .7694 HIMYFKGVPSRLGYLLDLAPKDLEKIIYFAAYVITSVDEEMRHNELSTLEAEMAVERK AVEDQRDGELEARAQKLEADLAELEAEGAKADARRKVRDGGEREMRQIRDRAQRELDR GLFCEKIFGPTRDWECYCGKYKRVRFKGIICERCGVEVTRAKVRRERMGHIELAAPVT similarity; putative" complement (7691. /protein_id="AAK44922. /db_xref="GI:13880219" /product="DNA-directed /note="similar to translation="MLDVNFFDELRIGLATAEDIRQWSYGEVKKPETINYRTLKPEKD/ /transl_table=11 /codon_start= SP:P37871; nd RNA polymerase, identified beta-prime subunit" уd

gene CDS

complement(7691. .8065) /gene="MT0697" /translation="MfDSAAATTNPGHAWASAMERSGLLECVAGLDEQPFGEFTADKLNPDRGSSRRVPRRQADGGIATHVERGGGQRQSGGQAGVVPQRMHGFPALAMQDRLIHHGEQTQNRIAQAFRVRFCVCSPT" /db_xref="GI:13880220" /translation="MPPC"/ppbpCC /gene="MT0697" /note="identified PF01261" /gene="MT0699" 10167. .10925 Glimmer2; putative; conserved authentic frameshift" complement(8058. /codon_start=1 /transl_table=11 /note="identified is not the result of a sequencing artifact; /gene="MT0698" /gene="MT0699" /note="This region contains an authentic frame shift .10925 .9972) bγ by Glimmer2; match to PFAM hypothetical protein, putative" protein family HMM identified by

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 3853)
1 (mboden, P., Troller, R., Marchesi, F., Telenti, A., Bodmer, T., Cole, S., Schopfer, K. and Burkart, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYCODACterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB) gene, Partial cds.
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                                                                                                               REPLEVEGILLOUGTDSFERILGSPRIKESAAERGDVNPVGGLEBUYELSPIEDESGS
MSLSFSDPREDDVKAPUDECKDKOMTYAAPLFVTAEFINNTGEIKSQTVFMGDEPMM
TEKGFFIINGTERVVVSQLVRSEGVYEDETIDKSTDKTLKSVKYIPSRGAWLEEDVDK
RDTVGVRIDKKRQPUYULKALGWTSBQIVEBRGESELMRSTLEKDNTVGTDEALLD
IYRKLREGEPTKESAQTYLENLEFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
EEDVVATIEYLVRLHEGQTTMTVPGGVEVPETDDIDIBFGNRELRTVCELIONQIRVG
MSRMERVVRERMITQDVEAITPOTLINIRTHVAAIKEFFGTSOLSGCMDQNNPLSGLT
HKRRLSALGFGGLSREKAGLEVRDVHDSHYGRWCPIETPEGPNIGLIGSLSVYARVNP
EGFIETPYRKVVDGVVSDGIVLTADEEDFVAAIKEFFGTSOLSGCMDQNNPLSGLT
FGFIETPYRKVTDGVVSDGIVLTADEDFAUNGANNGAVPLVREKAG
EVEYVPSSEVDYMDVSPRQMVSYATAMIPFLEHDDANRALMGANNGAVPLVREKAG
EVEYVPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANGAVPLVRESAP
LVGTGMELRAAIDATESSQESGVIEEVSADYITWHDNGTRRTYRMXFARSHGTC
VEEDVLTSIHIEHEIDARDTKLGAEEITRDIPNISDEVLADLDEGIVRIGAEVRD

DILVGKVTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGESGKVIGIRVFSRED
DILVGKVTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGESGKVIGIRVFSRED
EDELPRGVNELVRRYAQKKKISDGDKLAGRRGKGVIGKLIVAUEDMFFLADGTPVDI
TINTHRUDDBMNNTGOTT ETHIGENGAREVRDTSLKVPHGESGKVIGIRVFSRED
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                                        KLHHLVDDKIHARSTGPYSMITQQPLGGKAQFGGQRFGEMECWAMQAYGAAYTLQELLTIKS"
                                                                         ILNTHGVPRRMNIGQILETHLGWCAHSGWKVDAAKGVPDWAARLPDELLEAQPNAIVS
TPVFDGAQEAELQGLLSCTLPNRDGDVLVDADGKAMLFDGRSGEPFPYPVTVGYMYIM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /transi_table=11
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/protein_id="AAA20242.2"
/db_xref="GI-7144499"
/translation="MLEGCILADSROSKTAASPSPSRPQSSSNNSVPGAPNRVSFAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene=
576. .
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576. .>3853
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/strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="rpoB"
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Pred. No. 0.057;
Mismatches 0
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MSGRPOB/c
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TITLE
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Miller, L.P., Crawford, J.T. and Shinnick, T.M. The rpoB gene of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA polymerase beta-subunit; rpoB gene.
Mycobacterium tuberculosis (strain Rv) DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis RNA polymerase beta subunit (1 gene, complete cds and RNA polymerase beta subunit rpoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
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                                                                                                                                                                                            EEDVVATIEYLIKHLEGOTTHYTYPGGEVEPVEFTDIDHFGNRRLTTVGELLQNQIRVG
MSRMERVVRERWTTQDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMQNNPLSGLT
HKRRLSALGPGGLSRERAGLEVEDVHESHYGRWCPIETPEGPNIGLIGSLSVYARVNP
FGFIETPYRKVVDGVVSDEITVLTADEEDRHVVAQANSPIDADGRFVEERVLVRRKAG
EVEYVPSSEVDYMDVSPRQMVSYATAMIPFLEHDDANRALMGANMQRQAVPLYRRKAG
EVEYVPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMCRQAVPLYRRKAG
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LVGTGWELRAAIDAATSSSQESGVIEEVSADYITWHDNGTRTYRMRKFARSNHGTC
VEEDVLTSIHIEHEIDARDTRLGAEETTRDIPHISDEVLADLDERGIVRIGAEVRDG
LUCKVTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGSSGXVIGIKVSRED
EDELPAGVNELVRVYVAQKKKISDGDKLAGHHGNKGVIGKILPVEDMEFLADGTPVDI
ILNTHGVPRRNNIGQILETHLGWCAHSGWKVDAAKGVPDWAARLPDELLEAHANAIVS
TPVFDGAQEAELQGLLSCTLFWRDGDVLVDADGKAMLFDGRSGEPFPYPYTVGYMYIM
KLHHLVDDKTHARSTGPYSMITYQPPLGGKAQFFGGMRGGEMECWAMQAYGAAYTLQELL
TIKSDDTVGRVKYYEAIVKGENIFERGIPESKVLLKELQSLCLNVEVLSSDGAAIEL
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/transl_table=11
/product="RNA polymerase beta'-subunit"
/protein_id="AAA21417.1"
                                                                                                                         /gene="rpoC"
4641. .>5084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MLEGCILADSRQSKTAASPSPSRPOSSSNNSVPGAPNRVSFAKL REPLEVPGLLDVQTDSFEWLIGSPRWRESAAERGDVNPVGGLEEVLYELSPIEDFSGS MSLSESDPREDDVKAPVDECKDKDMTYAFDEFFKERFENNNTGEIKSQTVFKDFPMM TEKGTFIINGTERVVVSQLVRSPGVVFEDETLDKSTDKTLHSVXVIPSRGAVKLEFDVDK RDTVCVRIDRRRQPVTVLLKALGWTSEQIVERFGFSEIMRSTLEKDWTVGTDEALLD IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPTTSSTLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="rpoB"
1065. .4598
/gene="rpoB"
/codon_start=1
                                                                                                 1641. .>5084
/gene="rpoC"
                                                                       codon_start=1
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/protein_id="AAA21416.1"
/db_xref="GI:468334"
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/strain="Rv"
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.057;
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Gingeras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P
probniewski, F., Alland, D., Desmond, E., Holodniy, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gingeras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J. Simultaneous genotyping and species identification using hybridization pattern recognition analysis of generic mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA
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1 (bases 1 to 705)
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                             of microorganisms
Patent: US 6228575-A 24 08-MAY-2001;
                                                                             1 (bases 1 to 706)
Gingeras,T.R., Mack,D., Chee,M.S., Berno,A.J., Stryer,L.,
Ghandour,G. and Wang,C.
Chip-based species identification and phenotypic characterization
                                                                                                                                                                                            Unclassified
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20; Conser
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llarity 100.0%;
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/protein_id="AAC38533.1"
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/strain="ATCC27294"
/db_xref="ATCC:27294"
/db_xref="taxon:1773"
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/transl_table=11
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I50706
                                                          Highly conserved genes and their use to for detection of microorganisms patent: WO 0123604-A 2072 05-APR-2001; Infectio Diagnostic (I.D.I.) INC. (CA) Location/Qualifiers
                                                                                                                                                                    Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteriaceae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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Persing, D. H., Hunt, J.J., Young, K.K.Y.,
and Whelan, A.Christian.
Detection of a genetic locus encoding I
mycobacterial cultures and in clinical
patent: US 5643723-A 1 01-JUL-1997;
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Bergeron,M.G., Boissinot,M., Huletsky,A., m Nard,C.,
picard,F.J. and Roy,P.H.
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2072 from Patent WO0123604.
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227 c 250 g
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302 c 330 g
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            /strain="Rv"
/db_xref="taxon:1773"
                                    /organism="Mycobacterium tuberculosis"
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                                                                         Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N. Cleavage of nucleic acid acid using thermostable jannaschii FEN-1 endonucleases
Patent: US 5843669-A 138 01-DEC-1998;
Location/Qualifiers
                                                                                                                                              Unknown
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Sequence 138 from patent
AR062059
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Sequence 137
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Kalser, M.W., Lyamichev, V.I. and Lyamichev, N.
Cleavage of nucleic acid acid using thermostable methoanococcus
jannaschii FEN-1 endonucleases
Patent: US 5843669-A 137, 01-DEC-1998;
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Patent: US 5843669-A 136 01-DEC-1998;
Location/Qualifiers
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                                                                                                                                                                Unclassified.

1 (bases 1 to 620)

1 (bases 1 to 620)

Raiser,M.W., Lyamichev,V.I. and Lyamichev,N.

Cleavage of nucleic acid acid using thermostable methoanococcus
jannaschi FEN.1 endonucleases
Patent: US 5843669-A 140 01-DEC-1998;

Location/Qualifiers
      AF060353
Mycobacterium
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20; Conserv
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Cleavage of nucleic acid acid using thermostable methoanococcus
jannaschii FEN-1 endonucleases
Patent: US 5843669-A 139 01-DEC-1998;
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/trans1_table=11
/product="RNA polymerase beta subunit"
/protein_id="aAB59068:1"
/protein_id="aAB59068:1"
/db_xref="GI:149992"
/db_xref="GI:149992"
INIRPVVAAIKEFEGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDV
INIRPVVAAIKEFEGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDV
HPSHYGRMCPIETPEGPNIGLIGSLSVYARVNPFGFIETPYR"
                                                                                                                                                                                                                  /phenotype="rifampicin
/replace="t"
254
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mutation 234 G"
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/replace="a"
233
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232
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/replace="t"
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/replace="c"
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/replace="c"
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/replace="t"
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/replace="g"
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/replace="ca"
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DEFINITION
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FEATURES
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AR067448
AR067448.1
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                                                                                                                                                                                                                                                                            Kaiser M.W., Lyamichev, V.I. and Lyamichev, N.
Cleavage of nucleic acid acid using thermostable methoanococcus
jannaschii FEN-1 endonucleases
Patent: US 5843669-A 135 01-DEC-1998;
Location/Qualifiers
1. .620
                                                                                                                                                                                                                                                                                                                                                                                           tuberculosis
Patent: US 5851763-A 59 22-DEC-1998;
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Heym, B., Cole, S., Young, D., Zhang, Y.,
Bodmer, T.
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                                                                               Sequence 136 from patent AR062057
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1 (bases 1 to 620)
Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.
Cleavage of nucleic acid acid using thermostable methoanococcus
                                                                      AR062057.1
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                              Unclassified
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202 c 214 g
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Pred. No. 0.054;
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L05910 Mycobacter AR067448 Sequence

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Post-processing: Listing first 45 summaries
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Mycobacterium tuberculosis

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 432)

Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T., Colston,J., Matter,L., Schopfer,K. and Bodmer,T.

Detection of rifampicin-resistance mutation in Mycobacterium
                                        Antimicrob. Agents Chemother.
                                                                                                                                                                                                   Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin resistance gene, complete cds.
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    .432
    /organism="Mycobacterium tuberculosis"
/strain="H37"

                                Location/Qualifiers
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AE077396 Crithidia
247191 Calothrix
DAF080421 Agrocybe
AF080421 Agrocybe
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AR060353 Mycobacte
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AF172323 Bacillus
I50714 Sequence 9
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Z75951 Caenorhabdi
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3 Sequence 5 Sequence 7 Thermotog 5 Sequence 9 Sequence

Minimum Maximum

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Word size Searched:

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Result No.

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APPLICANT: JANNES, GEERT
APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: MASHINGTON
                                               Sequence Seq
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                      US-09-147-935A-5
US-09-147-935A-12
US-09-147-935A-14
US-09-147-935A-14
US-09-147-935A-19
US-09-147-935A-19
US-09-147-935A-24
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US-09-147-935A-30
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US-09-147-935A-35
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CLASSIFYCATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1657.0010000
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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APPLICANT: PORTAELS, FRAN OISE
APPLICANT: MACHTELINCKX, LIEVE
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-
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Matches 20; Conservative
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COUNTRY: US
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                                                    Compugen Ltd
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                   GenCore version 4.5
Copyright (c) 1993 - 2000 Comp
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Perfect score:
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Maximum I
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GENERAL INFORMATION:
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US-09-147-935A-41
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LENGTH: 306
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                                                                                                            Sequence 2, Application US/09147935A
| Patent No. 6242584
| GENERAL INFORMATION:
| APPLICANT: KOM, YOON-HOH
| APPLICANT: KOM, YOON-HOH
| TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
| TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF FROB GENE
| CURRENT APPLICATION NUMBER: US/09/147,935A
| CURRENT FILING DATE: 1999-03-19
| PRIOR FILING DATE: 1999-07-28
| NUMBER OF SEQ ID NOS: 50
| SOFTWARE: ROPATIN 1.0
| SEQ ID NO 2
| LENGTH: 306
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Fatent No. 6245584
Fatent No. 6245584
GENERAL INFORMATION:
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION:
TITLE OF INVENTION:
COMPARATIVE SEQUENCE ANALYSIS OF IPOB GENE
FILE REFERENCE: 0136/0F425
CURRENT FILING DATE: 1999-03-19
FRICK APPLICATION NUMBER: 05/09/147,935A
PRIOR APPLICATION NUMBER: 027-28
FILE REFERENCE: 1999-07-28
SOFTWARE: 1998-07-28
NUMBER OF SEQ ID NOS:
SOFTWARE: KOPATIN: 1.0
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ORGANISM: Mycobacterium africanum
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; ORGANISM: Mycobacterium bovis
US-09-147-935A-6
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| tacggtcggcgagctgatcc 24
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Best Local Similarity 100.(
Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserv
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US-09-147-935A-2
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US-09-147-935A-6
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US-09-147-935A-7
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LENGTH: 306
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US-09-147-935A-50
Sequence 50, Application US/09147935A
Patent No. 6242584
GENERAL INFORMATION:
APPLICANT: KOOK, YOOH-HOH
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF FOOB GENE
TITLE REFERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT APPLICATION NUMBER: PCT/KR98/00228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
APPLICANT: KOOK, Yoon-Hoh
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES E
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF TOB GENE
FILE REPERBENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR PILING DATE: 1999-03-19
PRIOR PILING DATE: 1998-07-28
SOFTWARE: 50
SOFTWARE: 600 NOS: 50
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Patent No. 6242584
GENERAL INFORMATION:
APPLICANT: KOOK, Yoon-Hoh
TILLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES FILE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF FOOB GENE TILLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF FOOB GENE GURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT APPLICATION NUMBER: PCT/KR98/00228
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR PLING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 50
SOFTMARE: AND NOS: 50
COMPANDED TO THE OF T
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100.0%; Pred. No. 0.24;
tive 0; Mismatches
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CRGANISM: Mycobacterium bovis BCG
US-09-147-935A-7
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Best Local Similarity 100;
Matches 20; Conservative
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Best Local Similarity
Matches 20; Conserv
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APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Honore, Nadine
APPLICANT: Homes
TITLE OF INVENTION: Rapid Detection of Antibiotic F
TITLE OF SEQUENTION: In Mycobacterium Tuberculosis
MINMER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-0CT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                  RESULT 8
US-09-082-614A-59
; Sequence 59, Application US/09082614A
; Patent No. 6124098
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
                                                                                                                                                                                                                                                                                                                                                                                                           Washington
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MOLECULE TYPE: DNA (genomic)
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TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
 18 TACGGTCGCCGAGCTGATCC 37
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                                                                                                                                                                     Heym, Beate
Cole, Stewart
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TYPE: nucleic acid
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Matches 20; Conservative
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APPLICANT: Heym,
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STATE: D.C
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APPLICANT:
APPLICANT:
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US-08-250-030-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance TITLE OF INVENTION: in Mycobacterium Tuberculosis NUMBER OF SEQUENCES: 66 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                     Score 20; DB 4; Length 306;
Pred. No. 0.24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 20; DB 2; Length 432;
Pred. No. 0.25;
; Mismatches 0; Indels
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SFILING PATE: 12-07-1994
FILING DATE: 12-07-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner STREET: 1300 I Street, N.W. CITY: Washington STATE: D.C.
                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REGISTRATION NUMBER: 25,146
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
INFOREMERAX: (202) 408-4400
INFOREMERAX: (202) 408-4400
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                            Mismatches
                                                                                                         ; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-50
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 59, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION:
APPLICANT: Heym, Beate
                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; P.
Matches 20; Conservative 0;
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100.0%;
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                                                                                                                                                                                                                                                             1 tacggtcggcgagctgatcc 20
                                                                                                                                                                                                                                                                                  1998-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Young, Douglas APPLICANT: Zhang, Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 432 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 100.0
Matches 20; Conservative
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                 NUMBER OF SEQ ID NOS:
SOFTWARE: KOPATIN 1.0
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PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        USA
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COUNTRY: UR
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APPLICANT:
                                   SOFTWARE:
SEQ ID NO 50
LENGTH: 306
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                                                                                           TYPE: DNA
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David H.
Detection of a Genetic Locus Encoding
Resistance to Rifampin in Mycobacterial Cultures and in
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                                         Gaps
                                         ö
100.0%; Score 20; DB 3; Length 432; 100.0%; Pred. No. 0.25;
                                         Indels
                                       ö
                                       Mismatches
                                                                                                                                                                                                                   Sequence 1, Application US/08250030
Patent No. 5643723
GENERAL INFORMATION:
APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of
TITLE OF INVENTION: Resistance t
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tacggtcggcgagctgatcc 20

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: KIM, BUN-JOON
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF FPOB GENE
FILE REPERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT APPLICATION NUMBER: PCT/KR98/00228
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR APPLIAND DATE: 1999-03-19
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: KOPATIN 1.0
SEQ ID NO 44
LENGTH: 306
                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                            100.0%; Score 20; DB 5; Length 970; 100.0%; Pred. No. 0.25; Live 0; Mismatches 0; Indels
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STATE: D.C.
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Pred. No.
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US-08-750-088A-30
Sequence 30, Application US/08750088A
SEQUENCE OF SECUENCE, HANS
APPLICANT: PORTAELS, FRAN OISE
APPLICANT: MACHTELINGKX, LIEVE
APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: METHOD FOR DETTITLE OF INVENTION: METHOD FOR DETTITLE OF INVENTION: RESISTANCE SPE
NUMBER OF SEQUENCES: 71
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOL
CORRESPONDENCE ADDRESS:
STERNE, KESSLER, GOL
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 11
US-09-147-935A-44
: Sequence 44, Application US/09147935A
: Patent No. 6242584
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100.0%; Pre
0; '
                                           TELEPHONE: 612-339-0331
TELEBRAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                          TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     261 TACGGTCGCCGAGCTGATCC 280
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Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity 100.
Matches 19; Conservative
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APPLICANT: MAYO FOUNDATION for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
SCHWEGMAN, Lundberg & Woessner
STREET: 3500 ILDS Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 20; DB 1; Length 970; 100.0%; Pred. No. 0.25; tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAMME: Mueting, Ann M.
REGISTRATION NUMBER: 150.105US1
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
                                                           ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
TITLE OF INVENTION: Clinical Specimens
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.105W01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application PC/TUS9506790 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 1: SEQUEBNCE CHARACTERISTICS: LENGTH: 970 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               261 TACGGTCGCCGAGCTGATCC 280
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Best Local Similarity
Matches 20; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: DNA. US-08-250-030-1
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                                                                                                                                            COUNTRY:
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PCT-US95-06790-1
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COUNTRY:

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Sequence 10, Application US/09147935A

Sequence 10, Application US/09147935A

Patent No. 6242584

GENERAL INFORMATION:
APPLICANT: KICH, BUM-JOON
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF TPOB GENE
TITLE OF INVENTION: O. COMPARATIVE SEQUENCE ANALYSIS OF TPOB GENE
TITLE OF INVENTION: U.36/06425
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 10
LENGTH: 306
                            APPLICANT: KIM, Bun-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
FILE REFERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
PRIOR FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS:
SOFTWARE: KOPATIN 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92.0%; Score 18.4; DB 4; Length 306; 95.0%; Pred. No. 1.5;
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                                                                                                                                                                                                                                                        ; SEQ ID NO 9
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium celatum Type2
US-09-147-9358-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA; ORGANISM: Mycobacterium chelonae
US-09-147-935A-10
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5 taccgtcggcgagctgatcc 24
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Best Local Similarity 95.0
Matches 19; Conservative
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              KOOK, Yoon-Hoh
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Best Local Similarity
Matches 19; Conserva
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APPLICANT: KIM, Bum-Joon
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
FILE REFERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR FILING DATE: 1998-07-28
PRIOR FILING DATE: 1998-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPOTER: IBM PC compatible
COMPOTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,088A
FILING DATE: 21-FEB-1997
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1657.001000
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 30: SEQUENCE CARRACTERISTICS: LENGTH: 25 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Mycobacterium aurum
US-09-147-935A-4
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Best Local Similarity 95.09
Matches 19; Conservative
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Best Local Similarity 95.0°
Matches 19; Conservative
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SOFTWARE: KOPATIN 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-08-750-088A-30
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US-09-147-935A-9
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US-09-147-935A-4
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LENGTH: 306
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US-08-01.

US-08-08-00

Sequence 70, Application US/08750088A

Patent No. 6602-0103.

GENERAL INFORMATION:

APPLICANT: DE BEENHOUWER, HANS

APPLICANT: MACHTELINKX, LIEVE

APPLICANT: MACHTELINKY, LIEVE

APPLICANT: MACHTELINKX, LIEVE

APPL
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Pred. No. 0.0027;
Mismatches 0; Indels
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ZIP: 20005-3934
COMPUTER REDABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-POS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,088A
                                                            US-09-147-935A-12
US-09-147-935A-14
US-09-147-935A-15
US-09-147-935A-16
US-09-147-935A-18
US-09-147-935A-17
US-09-194-759-754-1
US-09-094-759-3
US-09-094-359-5
US-09-094-359-5
US-09-094-359-9
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US-09-172-063-12
US-09-172-063-13
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NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1657,0010000
TELECOMMUTCATION INFORMATION:
TELEPHONE: 202-371-2540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: US/08/750,088A
21-FEB-1997
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Sequence 2, Appli
Sequence 6, Appli
Sequence 7, Appli
Sequence 41, Appli
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                                                                                                                                                                                                                                                  Search time 147.68 Seconds (without alignments) 33.266 Million cell updates/sec
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Sequence 43,
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US-09-147-935A-7
US-08-1313-1855-9
US-09-082-614A-59
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                                                                                                                                                                                                                                                      August 7, 2002, 21:52:14;
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RESULT 5
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US-09-147-935A-50
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GENERAL INFORMATION:

APPLICANT: KOOK, YOON-HOH

APPLICANT: KOOK, YOON-HOH

APPLICANT: KOOK, YOON-HOH

APPLICANT: KOOK, BUTTILE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY

TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF 100B GENE

FILE REPERENCE: 0136/07425

CURRENT APPLICATION NUMBER: US/09/147,935A

PRIOR APPLICATION NUMBER: DCT/KR98/00228

PRIOR APPLICATION NUMBER: PCT/KR98/00228

PRIOR APPLICATION NUMBER: DCT/KR98/00228

PRIOR APPLICATION NUMBER: DCT/KR98/00228

SOFTWARE: SOPTWARE: SOPTWAR
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Patent NO. 642584
GENERAL INFORMATION:
APPLICANT: KOOK, Yoon-Hoh
APPLICANT: KOM, Yoon-Hoh
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF TPOB GENE
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF TPOB GENE
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF TPOB GENE
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS:
SOFTWARE: KOPATIN 1.0
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                                                                                                                                                                                                                                                         ; Sequence 2, Application US/09147935A; Patent No. 6242584
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; ORGANISM: Mycobacterium africanum
US-09-147-935A-2
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Best Local Similarity 100.0
Matches 20; Conservative
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US-09-147-935A-2
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US-09-147-935A-6
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US-09-147-935A-7
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APPLICANT: KOOK, Yoon-Hoh
APPLICANT: KIM, BUM-DOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
FILE REPERBENCE: 0136/00F425
CURRENT APPLICATION NUMBER: 018/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR APPLICATION NUMBER: PCT/KR98/00228
NUMBER OF SEQ ID NOS: 50
SOFTWARE: KOPATIN 1.0
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APPLICANT: KOOK, YOON-HOH
APPLICANT: KOOK, YOON-HOH
APPLICANT: KOOK, YOON-HOH
APPLICANT: KIN, Bum-JOON
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF FDOB GENE
FILE REPRENCE: 0136/OF425
CURRENT APPLICATION NUMBER: US/09/147,935A
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR PPLICATION NUMBER: PCT/KR98/00228
PRIOR PPLICATION NOWE: 1998-07-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: KOPATIN 1.0
LENGTH: 306
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Patent No. 624284
GENERAL INFORMATION:
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: A METHOD FOR IDENTIFYING WYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
FILE REFRENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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100.0%; Pred. No. 0.0022;
iive 0; Mismatches 0;
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; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; Sequence 41, Application US/09147935A ; Patent No. 6242584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Mycobacterium bovis BCG
US-09-147-935A-7
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Best Local Similarity 100.
Matches 20; Conservative
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Best Local Similarity 100.(
Matches 20; Conservative
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David H. Detection of a Genetic Locus Encoding Resistance to Rifampin in Mycobacterial Cultures and in
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APPLICANT: Telenti, Amalio
APPLICANT: Telenti, Amalio
APPLICANT: Redenti, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
CORRESPONDENCE: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 432;
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                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Finnegan, Henderson, Farabow, Garrett
ADDRESSEE: Dunner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 20; DB 3; 1
100.0%; Pred. No. 0.0022;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERCE/FOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                                                                             Sequence 59, Application US/09082614A Patent No. 6124098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1, Application US/08250030
; Patent No. 5643723
; GENERAL INFORMATION:
APPLICANT: Persing, David H.
TITLE OF INVENTION: Resistance t
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            18 TACGGTCGGCGAGCTGATCC 37
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Zhang, Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 5
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
                                                                                                                                                                                      Heym, Beate
Cole, Stewart
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 20005-3315
                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                  Zhang,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Wash:
STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE
                                                                                      RESULT 8
US-09-082-614A-59
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APPLICANT:
APPLICANT:
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APPLICANT: Honore, Nadine
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Telenti, Amalio
APPLICANT: Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                     Score 20; DB 4; Length 306;
Pred. No. 0.0022;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: DESTEM: CONTROLDE SOFTWARE: PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA: PATENTIN NUMBER: US/08/313,185 FILING DATE: 12-OCT-1994 ATTONEY/AGENT TEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Meyers, Kenneth J.
REGIGYRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                       ) ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-50
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 59, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
SOFTWARE: PatentIn Release #
                                                                                                                                                                                                       100.0%;
100.0%;
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PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: KOPATIN 1.0
                                                                                                                                                                                                                                                                                       1 tacggtcggcgagctgatcc 20
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Conservative
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Cole, Stewart
Young, Douglas
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Best Local Similarity 100.(
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Washington
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Best Local Similarity
Matches 20; Conserv
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ZIP: 20005-3315
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APPLICANT:
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                                                               SEQ ID NO 50
LENGTH: 306
                                                                                                        TYPE: DNA
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Gaps

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Sequence 44, Application US/09147935A

Patent No. 624258

GENERAL INFORMATION:
APPLICANT: KOOK, Yoon-Hoh
APPLICANT: KIM, Bum-Joon
ITILE OF INVENIION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENIION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENIION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENIION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENIION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS:
SOFTWARE: KOPATIN 1.0
SEQ ID NO 44
LENGTH: 306
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Fatent No. 6329138
GENERAL INFORMATION
APPLICANT: DE BEENHOUWER, HANS
APPLICANT: MACHTELINCKX, LIEVE
APPLICANT: MACHTELINCKX, LIEVE
APPLICANT: ANNES, GERT
APPLICANT: APPLICANT: ANNES, GERT
TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
CORRESPONDENCE ADDRESS:
ADDRESSE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
                                                                                                                                                                                                                                                                                                               100.0%; Score 20; DB 5; Length 970; 100.0%; Pred. No. 0.0021; Live 0; Mismatches 0; Indels
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Pred. No. 0.0084;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                  TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
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100.08; Pre
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US-09-147-935A-44
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Matches 19; Conservative
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Best Local Similarity
Matches 20; Conserv
                                                                                                                                                          ; TYPE: nucleic s
; STRANDEDNESS:
; TOPOLOGY: lines
; MOLECULE TYPE: DN
PCT-US95-06790-1
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US-09-147-935A-44
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US-08-750-088A-30
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GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
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MEDIUM TYPE: Floppy disk
COMPUTER: Eleopy disk
COMPUTER: Eleopy disk
COMPUTER: THE PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/250,030
FILING DATE: 26-MAY-1994
CLEASIFICATION SATE: 33-50
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 150.105US1
TELEPHONE: 612-339-031
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LEMOTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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ZIP: 55402

COMPOTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC Compatible

COMPRATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/06790

FTLING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 20; Conservative 0; Mismatches 0;
                                                                   SEE: Schwegman, Lundberg & Woessner: 3500 IDS Center
Minneapolis
TITLE OF INVENTION: Clinical Specimens
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NAME: Raasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.105W01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 TACGGTCGGCGAGCTGATCC 280
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                       NUMBER OF SEQUENCES: 1:
CORRESPONDENCE ADDRESS:
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                                                                                                                                                            USA
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; MOLECULE TYPE:
US-08-250-030-1
                                                                                                                                STATE: MN
COUNTRY: U
                                                                                                                                                                                 55402
                                                                 ADDRESSEE:
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PCT-US95-06790-1
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Gaps

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COUNTRY:

Length 306;

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Sequence 30, Application US/08750088A Patent No. 6329138 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Sequence 44, Application US/09147935A
; Patent No. 6242584
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               95.0
100.08; Pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DE BEENHOUWER, HANS
APPLICANT: PORTAELS, FRAN OISE
APPLICANT: MACHTELINCKX, LIEVE
    TELECOMMUNICATION INFORMATION: TELEPHONE: 612-339-0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Mycobacterium xenopi
US-09-147-935A-44
                                                                                                                                                                                                                                                                                                                                                                                 261 TACGGTCGGCGAGCTGATCC 280
                                                                                                                                                                                                                                                                                                                                           1 tacggtcggcgagctgatcc 20
                                         TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 100.
Matches 19; Conservative
                                                                                                     LENGTH: 970 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: KOOK, YOON-HOH
APPLICANT: KIM, Bum-Joon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 7.
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, KI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WASHINGTON
                                                                                                                                                                 linear
                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                    MOLECULE TYPE:
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US-08-750-088A-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-147-935A-44
                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO 44
LENGTH: 306
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUBER: US/08/250,030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
ELLING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match

100.0%; Score 20; DB 1;
Best Local Similarity 100.0%; Pred. No. 0.0021;
Matches 20; Conservative 0; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
CITY: Minneapolis
                STREET: Schwegman, Lundberg & Woessner STREET: 3500 IDS Center CITY: Minneapolis STATE: MN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Raasch, Kevin W.
RECISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150.105w01
TITLE OF INVENTION: A Clinical Specimens NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                              150.105US1
                                                                                                                                                                                                                         COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/POCKET NUMBER: 150.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                261 TACGGTCGCCGAGCTGATCC 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 tacggtcggcgagctgatcc 20
                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 970 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COUNTRY: U
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                                                                                                                                               COUNTRY:
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CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR FILING DATE: 1999-03-19
RIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 50
SOFTWARE: KOPATIN 1.0
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                                                            Gaps
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  Length 970;
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Pred. No. 0.0084;
0; Mismatches 0; Indels
Query Match 100.0%; Score 20; DB 5; Length 97 Best Local Similarity 100.0%; Pred. No. 0.0021; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            E: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
1100 NEW YORK AVENUE, SUITE 600
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1998-07-28

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APPLICANT: Honore, Nadine
APPLICANT: Honore, Nadine
APPLICANT: Telaniso
APPLICANT: Tolomer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                          Length 306;
                                                                                                                                                                                               Query Match 100.0%; Score 20; DB 4; Length 30 Best Local Similarity 100.0%; Pred. No. 0.0022; Matches 20; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: D.C.
COMPUTER EADABLE FORM:

ZIP: 20005-1315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTHWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
TASSTELCATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
                                                                                                ; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-50
                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 59, Application US/08313185
Patent No. 5851763
GENERAL INFORMATION
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Dunner
1300 I Street, N.W.
                                                                                                                                                                                                                                                                                1 tacggtcggcgagctgatcc 20
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TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 432 base pairs
TYPE: nucleic acid
PRIOR EILING DATE: 1998-0
NUMBER OF SEQ ID NOS:
SOFTWARE: KOPATIN 1.0
SEQ ID NO 50
LENGTH: 306
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                             US-08-313-185-59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
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David H.
Detection of a Genetic Locus Encoding
Resistance to Rifampin in Mycobacterial Cultures and
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0
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APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 20; DB 3; Length 432; 100.0%; Pred. No. 0.0022; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                       Finnegan, Henderson, Farabow, Garrett &
                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 2005-3315
COMPUTER RADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/313,185
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: MCAPERS, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELEPHONE: (202) 408-4000
TELEPHONE: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
US-09-082-614A-59; Sequence 59, Application US/09082614A; Patent No. 6124098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08250030
Patent No. 5643723
GENERAL INFORMATION:
APPLICANT: Persing, David H.
TITLE OF INVENTION: Detection of
TITLE OF INVENTION: Resistance t
                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Finnegan, Hender
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: DNA (genomic)
US-09-082-614A-59
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                                                                                                                                                  Zhang, Ying
Honore, Nadine
                                                                                         Heym, Beate
Cole, Stewart
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 432 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.
Matches 20; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                  CITY: Wash
STATE: D.C
                                                                                                                                                                      APPLICANT:
                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 9
US-08-250-030-1
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100.0%; Score 20; DB 2; Length 432; larity 100.0%; Pred. No. 0.0022; Conservative 0; Mismatches 0; Indels

Query Match Best Local Similarity Matches 20; Conserv

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Sequence 10, Application US/09147935A

Patent No. 6242584

GENERAL INFORMATION:

APPLICANT: KOOK, YOON-HOH

APPLICANT: KOOK, YOON-HOH

TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF FDOB GENE

TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF FDOB GENE

FILE REFERENCE: 0136/0F425

CURRENT FILING DATE: 1999-03-19

PRIOR FILING DATE: 1998-07-28

NUMBER OF SEQ ID NOS: 50

SOFTWARE: KOPATIN 1.0

LENGTH: 306
              APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF 100B GENE
FILE REFERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: 0.5/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR96/00228
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 50
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0.46;
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Job time: 7171 sec
                                                                                                                                                                                                                                        EBNGTH: 306
TYPE: DNA
ORGANISM: Mycobacterium celatum Type2
US-09-147-935A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; TYPE: DNA
; ORGANISM: Mycobacterium chelonae
US-09-147-935A-10
                                                                                                                                                                                                                                                                                                                                                                 Query Match 80.0
Best Local Similarity 100.
Matches 16; Conservative
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Best Local Similarity 100.
Matches 16; Conservative
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KOOK, Yoon-Hoh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-147-935A-10
                                                                                                                                                                                                                       SEQ ID NO 9
APPLICANT:
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Sequence 4, Application US/09147935A

Sequence 6.242584

GENERAL INFORMATION:

APPLICANT: NOOK, YOON-HOh

TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY

TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE

TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF FOR GENE

TITLE OF INVENTION: UNMBER: US/09/147,935A

CURRENT APPLICATION NUMBER: US/09/147,935A

CURRENT FILING DATE: 1999-03-19

PRIOR PILING DATE: 1998-07-28

NUMBER OF SEQ ID NOS: SOFTWARE: KOPATIN 1.0
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          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,088A
FILING DATE: 21-FEB-1997
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 16; DB 4;
Pred. No. 0.46;
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100.0%; Pred. No. v
0; Mismatches
                                                                                                                                                                                           ATTORNEY AGENT INFORMATION:
NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1657.0010000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 25 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA
CRGANISM: Mycobacterium aurum
US-09-147-935A-4
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Best Local Similarity 100.
Matches 16; Conservative
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US-08-750-088A-30
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Best Local Similarity
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US-09-147-935A-9
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US-09-147-935A-4
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LENGTH: 306
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August 7; 2002, 23:51:48; Search time 147.68 Seconds (without alignments) 33.266 Million cell updates/sec
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
GenCore Version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-09-147-935A-6
US-09-147-935A-7
US-09-147-935A-41
US-09-147-935A-59
US-08-313-185-59
US-08-250-030-1
PCT-US95-06790-1
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US-09-147-935A-31
US-09-147-935A-31
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US-08-750-088A-30
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Maximum DB seq length: 200000000
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Match Length DB
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Perfect score:
Sequence:
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Sequence 2, 8 Sequence 10, 8 Sequence 10, 8 Sequence 1, Ap Sequence 43, 8

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US-09-103-840A-2 US-09-103-840A-1

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9-426-998-4 7-612-674-11 9-147-935A-12 9-147-935A-14 9-147-935A-16 9-147-935A-16 9-147-935A-16 9-147-935A-17 9-147-935A-17 9-109-637A-22 8-506-404D-1 9-035-754-1 9-035-754-1 9-094-359-3 9-094-359-3 9-094-359-3 9-094-359-7 9-172-063-11	ALIGNMENTS NS SE VE CE SPECTRUM OF CE SPECTRUM OF TE SPECTRUM OF TO, Version TO, Version TO, 088A TO, 088A TO, 010000	Score 20; D Pred. No. 0. Mismatches
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7741 279 306 306 306 306 306 720 720 720 720 720 720	T. 1 1.750.088A-70 UUROCC 70, APPLICATION US/08750088 APPLICANT: DE BENHOUWER, HANS APPLICANT: DE BENHOUWER, HANS APPLICANT: PORTBELS, FRN OISE APPLICANT: PORTBELS, FRN OISE APPLICANT: ROSSAU, RUID TITLE OF INVENTION: METHOD FOR D TITLE OF INVENTION: RESISTANCE S ADDRESSEE: STENE, KESSLER, GC STREET: 1100 NEW YORK AVENUE, STRATE: D.C. COUNTRY: WASHINGTON APPLICANT: BM PC COMPATIBLE COMPUTER: BM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DC SOFTWARE: PLOPPY disk COMPUTER: BM PC COMPATIBLE COMPUTER: BM PC COMPATIBLE OF STATE: 2005-3934 CLASSIFICATION DATA: 32005-3934 CLASSIFICATION NUMBER: US/08/750, FILING DATE: \$21-FEB-1997 CLASSIFICATION NUMBER: 29,021 REFERENCE/DOCKET NUMBER: 26,02 TELECOMMUNICATION: NUMBER: 29,021 TELECHONE: 202-371-260 FFORMATION FOR SEQ ID NO: 70: SEQUENCE CHARACTERISTICS: LENGTH: 20 base pairs TYPE: nucleic acid STRANDEDRESS: single TOPOLOGY: linear MOLECULE TYPE: CDNA	100 .larity 100 Conservative
	1 750-088A-70 ence 70, Application nt No69291091 ERAL INFORMATION: PPLICANT: DE BERHOU PPLICANT: DORTAELS, PPLICANT: MACHTEINS, PPLICANT: MACHTEINS, PPLICANT: MACHTEINS, PPLICANT: MACHTEINS ITLE OF INVENTION: MITLE OF INVENTION: MITLE OF INVENTION: MITLE OF INVENTION: MITLE OF INVENTION: MACHTEINS CITY: WASHINGTON STRAE: D.C. COUNTRY: US ZIP: 20005-3934 OMPUTER READABLE FORM MEDIUM TYPE: FLOOPY COMPUTER: IBM PC COUNTRY: US SOFTWARE: PATENTION NUMBER: FILING DATE: %21-FEB CLASSIFICATION NUMBER: TTCANEY/AGENT INFORMANNEY TTCASIFICATION INFORMANTION FOR SEQ ID INFORMATION FOR SE	/ rva1
00000000000000000	TON: 1001: 100	/ Match Local Similarity nes 20; Conser
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	T 1 1-750-08 uence 7 went 10 APPLICA CONNT TELECO APPLICA TELECO	Mat
22888888888888888888888888888888888888	SULT 1 -08 750-088A-70 Sequence 70, Application US/0875008 Patent No_69293938 APPLICANT: DE BEENHOUWER, HANS APPLICANT: PORTAELS, FRAN OISE APPLICANT: PORTAELS, FRAN OISE APPLICANT: PORTAELS, FRAN OISE APPLICANT: ROSSAU, RUDI TITLE OF INVENTION: METHOD FOR TITLE OF INVENTION: RESISTANCE: ADDRESSE: STREE; D.C. COUNTRY: USA SEQUENCES: 71 CONTRY: WASHINGTON ORW YORK AVENUE, CITY: WASHINGTON OR TITLE OF INVENTION: WASHINGTON OR TOO ON THE SECONDALISE FORM: MEDIUM TYPE: Floppy disk COMPUTER: EMP PC COMPATION: MEDIUM TYPE: Floppy disk COMPUTER: Patentin Release #1 CURRENT APPLICATION DATA: APPLICATION: NUMBER: US/08/750 FLING DATE: %21-FEB-1997 CLASSIFICATION: %21-EB-1997 CLASSIFICATION: NUMBER: 29,021 REFERENCE/DOCKET NUMBER: 1657 TELECHONE: 20-371-260 INPORMATION FOR SEQ ID NO: 70: SEQUENCE CHARACTERISTICS: LENGTH: 20 base pairs TYPE: nucleic acid STRANDEDNESS: single MOLECULE TYPE: CDNA	Query Match Best Local Matches 2
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; Sequence 50, Application US/09147935A ; Patent No. 6242584
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; ORGANISM: Mycobacterium bovis BCG
US-09-147-935A-7
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Matches 20; Conservative
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APPLICANT: KOOK, YOON-HOH
APPLICANT: KIM, Bum-JOON
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US-09-147-935A-50
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LENGTH: 306
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APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF TOOB GENE
FILE REFERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT APPLICATION NUMBER: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR FILING DATE: 1998-07-28
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APPLICANT: KOOK, YOON-HOH
APPLICANT: KIM, BUM-JOON
ATILLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPE
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF, rpoB GENE
TITLE REFERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-07-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
NUMBER OF SEQ ID NOS:
SOFTWARE: KOPATIN 1.0
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                                                                                                                                      Sequence 2, Application US/09147935A Patent No. 6242584
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; TYPE: DNA
; ORGANISM: Mycobacterium africanum
US-09-147-935A-2
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Matches 20; Conservative
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SOFTWARE: KOPATIN 1.0
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                                                                                                                 US-09-147-935A-2
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US-09-147-935A-7
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APPLICANT: KOOK, YOON-BOA
APPLICANT: KIM, Bum-JOON
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rpoB GENE
FILE REFERENCE: 0136/OP425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT APPLICATION NUMBER: D99-03-19
PRIOR FILING DATE: 1999-07-28
SOFTWARE: KOPATIN 1.0
SEQ ID NO 7
LENGHARE: 306
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APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF TPOB GENE
FILE REFERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-07-319
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR APPLICATION NUMBER: PCT/KR98/00228
WINMER OF SEQ ID NOS:
SOFTWARE: SOFTWARE: 50
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CURRENT APPLICATION NUMBER: 1059-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
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100.0%; Score 20; DB 4; I
Best Local Similarity 100.0%; Pred. No. 0.0022;
Matches 20; Conservative 0; Mismatches 0;
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; Patent No. 6242584
; GENERAL INFORMATION:
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0136/0F425
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Best Local Similarity 100.8
Matches 16; Conservative
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Best Local Similarity 100.
Matches 16; Conservative
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APPLICANT: KOOK, YOON-HOH
APPLICANT: KIM, Bum-JOON
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SOFTWARE: KOPATIN 1.0
SEQ ID NO 10
LENGTH: 306
                                 Bum-Joon
                             APPLICANT: KIM, Bum-
TITLE OF INVENTION:
TITLE OF INVENTION:
FILE REFERENCE: 0136
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US-09-147-935A-10
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TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF TPOB GENE
FILE REPERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT APPLICATION NUMBER: US/09/147,935A
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR ELING DATE: 1998-07-28
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100.0%; Pred. No. v.
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NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1657.0010000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFRAX: 202-371-2540
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US-09-147-935A-4
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Matches 16; Conservative
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APPLICANT: KOOK, YOON-HOh
APPLICANT: KIM, Bum-Joon
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US-08-750-088A-30
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SOFTWARE: KOPATIN
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US-09-147-935A-9
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A METHOD FOR IDENTIFYING MYCOBACTERIAL SP
COMPARATIVE SEQUENCE ANALYSIS OF TPOB GENE
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                                                                                                                                                                                                                                                                                                                    Length 306;
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                                                 CURRENT APPLICATION NUMBER: US/09/147,935A CURRENT FILING DATE: 1999-03-19 PRIOR APPLICATION NUMBER: PCT/KR98/00228 PRIOR FILING DATE: 1998-07-28 NUMBER OF SEQ ID NOS: 50 SOFTWARE: KOPATIN 1.0 LENGTH: 306
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; ORGANISM: Mycobacterium celatum Type2
US-09-147-935A-9
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; ORGANISM: Mycobacterium chelonae
US-09-147-935A-10
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Perfect score:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Result No.

Score

Query Match Length DB

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Description

SUMMARIES

RESULT 1 AF057450 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS	c c 222 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	11100000000000000000000000000000000000
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inear BCT 17-SEP-1999 (rpoB) gene, partial bacteridae: eriaceae; mmplex. G.H., Chae,G.T., comparative sequence	A47816 Sequence 30 AXD50338 Sequence AE000976 Mycobacte AF057459 Mycobacte AF057459 Mycobacte AF057460 Mycobacte AF057471 Mycobacte AF057471 Mycobacte AF057473 Mycobacte AF057473 Mycobacte AF057479 Mycobacte AF057479 Mycobacte AF157010 Sequence AR157011 Sequence AR157012 Sequence AR157021 Sequence AR157024 Sequence AR157024 Sequence AR157025 Sequence AR157026 Sequence AR157030 Sequence AR157040 Sequence	AF057450 Mycobacte AF057451 Mycobacte AF057452 Mycobacte AF057453 Mycobacte AF057454 Mycobacte AF157007 Sequence AR157008 Sequence AR157008 Sequence AR157051 Sequence AR157051 Sequence AR157051 Sequence AR157051 Sequence 105910 Mycobacteri AR067448 Sequence 150706 Sequence

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JOURNAL
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AUTHORS
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                                                                                                                                                                    Submitted (06-APR-1998) Microbiology, College of Medicine, 28 Youngon-dong,
                                                                                                                                                                                                    2 (bases 1 to 306)
Kook,Y.H., Kim,B.J., Lee,S.H.,
Kim,S.J., Chae,G.T., Kim,E.J. &
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium bovis.
Mycobacterium bovis
Bacteria, Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                            Kim.B.J. Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T., Kim,B.C., Cha,C.Y. and Kook,Y.H.
Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
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1 95 c 108 g 47 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 306)
Kook, Y.H., Kim, B.J., Lee, S.H., Lyu, M.A., Kim, S.
Kim, S.J., Chae, G.T., Kim, E.J. and Cha, C.Y.
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Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
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95 c 108 g 47 t
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KIM,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,

Kim,E.C., Cha,C.Y. and Kook,Y.H.

Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)

J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

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Mycobacterium tuberculosis.

Mycobacterium tuberculosis
Bacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
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Submitted (06-APR-1998) Microbiology, Seoul National University
College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 (bases 1 to 306)
Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., KKim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
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Method for identifying mycobacterial sequence analysis of rpoB gene Patent: US 6242584-A 2 05-JUN-2001; Location/Qualifiers
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Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)

J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
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Rook, Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.

Direct Submission

Submitted (06-APR-1998) Microbiology, Seoul National University College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
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/product="RNA polymerase beta"
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/strain="H37Rv; ATCC27294"
/db_xref="ATCC:27294"
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Sequence 41 from patent US 6242584.
AR157042
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Rook, y.-H. and Kim, B.-J.

Method for identifying mycobacterial species sequence analysis of rpoB gene Patent: US 6242584-A 6 05-JUN-2001;
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                Telenti,A., Imboden,P., Marchesi,F., Lowrie, Colston,J., Matter,L., Schopfer,K. and Bodme Detection of rifampicin-resistance mutation
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           tuberculosis
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Kook,Y. and Kim,B.

Kook,Y. and Kim,B.

Method for identifying mycobacterial species by comparative sequence analysis of rpoB gene Patent: US 624584-A 50 05-JUN-2001;
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Sequence 50 from patent US
AR157051 GI:15125755
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1. .306
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94 c 108 g
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95 c 108 g
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                               , Marchesi, F., Lowrie, D., Cole, S.T.,
Schopfer, K. and Bodmer, T.
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subunit; rifampicin
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TACGGTCGGCGAGCTGATCC
            tacggtcggcgagctgatcc 20
                                                 h 100.0%;
Similarity 100.0%;
20; Conservative 0;
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                                                                                                                                                                         /phenotype="rifampicin
/replace="t"
254
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/protein_id="AAB59068.1"
/db_xref="GI:149992"
/db_xref="GI:149992"
/translation="GURERRYUGELIQNQIRYGMSRMERVVRERMTTQDVEAITPQTL
INIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDV
HPSHYGRMCPIETPEGPNIGLIGSLSVYARVNPFGFIETPYR"
                                                                                                                              /phenotype="rifampicin
/replace="c"
140 c 148 g
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/replace="g"
232
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247. .248
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/strain="H37"
/db_xref="taxon:1773"
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/replace="a"
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/replace="t"
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                                                 Score 20; DE
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                            AX111339
Sequence
AX111339
                                                                                                                                                                                                                                          Unclassified.

1 (bases 1 to 970)

1 (bases 1 to 970)

1 (pases 1 to 970)

Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.A., and Whelan,A.Christian.

Detection of a genetic locus encoding resistance to rmycobacterial cultures and in clinical specimens Patent: US 5643723-A 1 01-JUL-1997;
                                                                                                                                                                                                                                                                                                                                                         I50706
Sequence 1 from
I50706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rapid detection of antibiotic resistance tuberculosis
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Sequence 59 from paten1
AR067448
AR067448.1 GI:5998670
                                                                                                                                                                                                                                                                                                                  Unknown
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                    AX111339.1
                                                                                                                                                                                                                                                                                                                            Unknown
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1 (bases 1 to
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2072 from Patent W00123604
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1. .970
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1. .432
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139 c 149 g
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302 c 330 g
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Mycobacterium tuberculosis H37Rv RNA-polymerase beta
gene, partial cds.
U12205
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1 (bases 1 to 3853)
Imboden, P., Troller, R., Marchesi, F., Telenti, A., B Cole, S., Schopfer, K. and Burkart, T.
The rpoB gene of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium tuberculosis.

Mycobacterium tuberculosis

Mycobacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 3534)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
Submilted (11-UUL-1994) Paul Imboden, Institute for Medical Microbiology, University of Berne, Friedbuehlstrasse 51, Ber 3010, Switzerland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           U12205.1 GI:515684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Imboden, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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/Product="RNA-polymerase beta subunit"
/Product="RNA-polymerase beta subunit"
/protein_id="AAA20242.2"
/protein_id="AAA20242.2"
/db_xref="GI:7144499"
/db_xref="GI:7144499"
/translation="MLEGCILADSRQSKTAASPSPSRPQSSSNNSVPGAPNRVSFAKL
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TEKGTFIINGTERVVVSGLVRBGGVYEDETIDKSTDKTLHSVKVIPSRGAWLEFDVDK
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                                                                                                                                                                                                                                                                 /gene=
                                                                                                                                                                                                                                                                                                         /db_xref="taxon:1773"
576. .>3853
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                                                                                                                                                                                                                                           'gene="rpoB"
                                                                                                                                                                                                                                                                                                                                                     /strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mycobacterium tuberculosis"
/strain="Rv"
                                                                                                                                                                                                                                                                                                                                                                    ∕organism="Mycobacterium
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MSRWERVVRERMTTQDVEAITPGTLINIRPVVAAIKEFFGTSQLSQFMQONNPLSGLT
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TIKS"

723 a 1173 c 1293 g 664 t
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Query Match 100.0%; Score 20; DB 1; Length 3853; Best Local Similarity 100.0%; Pred. No. 3;

BASE COUNT ORIGIN

Matches

Conservative

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Search completed: August 7, 2002, 23:49:01 Job time: 9215 sec

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AT2558. AT25548. AT25583.

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                                                                                                                                                                             TITLE
                                                                                                                                                                                                      AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                           source
                                                                                                         Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 510559573
Fax: 5105595818
                                                                                                                                                                  Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D. The structure and function of the expressed portion of the wheat genomes. Normalized root cDNA library
                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticeae; Triticum.

1 (bases 1 to 422)
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Triticum aestivum
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                                                                 quality sequence with phred score less
Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                          Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
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/db_xref="taxon:4565"
/clone="WHE1122_B06_C12"
/tissue_type="Root"
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AV197881 AV197881
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;

; Triticeae; Triticum.

1 (bases 1 to 544)

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hala,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,

Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector
quality sequence with phred score less than
Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genomes - Normalized root cDNA library Unpublished (2000)
Contact: Olin Anderson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BE445100 544 bp mRNA linear EST 25-JUL-: WHE1132_H08_P16ZS Wheat etiolated seedling root normalized cDNA library Triticum aestivum cDNA clone WHE1132_H08_P16, mRNA
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/db_xref="taxon:4565"
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/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
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                                                                                                     'tissue_type="Root"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ocation/Qualifiers
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/lab_host="E. coli DH10B"
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AUTHORS
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LOCUS
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(Coases 1 to 558)

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han, P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library

Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                     Sequence have been trimmed to remove vector quality sequence with phred score less than Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triticum aestivum
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                                                                                                                                                                                                                                                                                                                                                                                                                   oandersn@pw.usda.gov
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds
                                                                                                                                                                                     /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1137_H03_005"
                                                                                                             /tissue_type="Root"
                                                                                                                                                  /clone_lib="Wheat etiolated seedling root normalized cDNA
                                                                                                                                                                                                                                                                ∕organism="Triticum aestivum"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Wing RA
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
The Tordan Hall, Clemson, SC 29634, U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library Unpublished (2001)
On Jun 26, 2000 this sequence version replaced gi:13187931.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BE195103 610 bp mRNA linear EST 22-OCT-2001
HVSMEh0088E21f Hordeum vulgare 5-45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0088E21f,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BE195103
                                                                                                                                                                                                                                                                                                                                                                                                   Total hq bases = 238
Seq primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 864 656 7288
Fax: 864 656 4293
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystalization dishes. Roots were harvested: The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before
/note-"Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spikes with awns trimmed were collected at 5, 10, 15, 20,
                                                                                                                                  /clone_lib="Hordeum vulgare 5-45
HVcDNA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
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                                                                                                                                                                                                               /cultivar="Morex"
/db_xref="taxon:4513"
/clone="HVSMEh0088E21f"
                                                                                                           /lab_host="SOLR"
                                                                                                                                                                                                                                                                                             organism="Hordeum vulgare"
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                                                                                                                                                                                                                            Email: oandersn@pw.usda.gov
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence
Sequence have been trimmed score less than 20
                                                                                                                                                                                                                                                                                                                                                  Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsla,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat
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                                                                                                                                                                                                    quality sequence with phred score less than Seq primer: Stratagene SK primer.
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BE442518
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)
a 203 c 158 g 120 t
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                              /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1101_H10_O19"
                                                                                                                  /organism="Triticum aestivum"
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/clone_lib="Wheat etiolated seedling root normalized
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Pred. No.
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                                                                                                                                                                                                   Email: rwing@clemson.edu
Total hg bases = 574
Seq primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 643.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Henry, D., Palmer, M., Rambo, T., Simmons, J., Oates, R., Choi, D.W., Fenton, R.D. and Main, D.

Development of a genetically and physically anchored EST resource for barley genomics: Morex cold-stressed seedling shoot cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BG299722 828 bp mRNA linear EST 17-OCT-2001
HVSMEa0021120f Hordeum vulgare seedling shoot EST library
HVCDNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0021120f.
                                                                                                                                                                                                                                                                                                                                   Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                               Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hordeum vulgare
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
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                        /clone_lib="Hordeum vulgare seedling shoot
HVcDNA0001 (Cold stress)"
                                                                          /db_xref="taxon:4513"
/clone="HVSMEa0021I20f"
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/tissue_type="Seedling shoot"
                                                                                                                                /cultivar="Morex"
                                                                                                                                                /organism="Hordeum vulgare"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before
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/dev_stage="Five day old etiolated seedling"
/dev_stage="Five day old etiolated seedling"
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                                                                                                                                                                                                                                                                                                           Contact: Turkewitz AP
Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BM397871 130 bp mRNA linear EST 17 5009-0-38-C10.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.
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17; Conserv
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EST from Tetrahymena thermophila, strain CU428.1, growing cells
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                                                                                                                                                                                                                   Seq primer: T3
                                                                                                                                                                                                                                                                        Tel: 773 702 4374 Fax: 773 702 3172
                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 130)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orlas,E., Kirk,K.E., Frankel
                                                                                                                                                                                                                                         Email: apturkew@midway.uchicago.edu
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/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol;
Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 50c for 2 days. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 600000 pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begun, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
/organism="Tetrahymena thermophila"
/strain="QU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                this clone see http://www.genome.clemson.edu/orders Al see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchors EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" a 271 c 220 g 165 t
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http://www.genome.clemson.edu/projects/barley.
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  in Chilcoat and Turkewitz (2001)
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Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
                                                                                                             BM398255 134 bp mRNA linear 5009-0-42-H08.t.1 Chilcoat/Turkewitz cDNA (large
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Turkewitz AP
Molecular Genetics and Cell Biology
University of Chicago
920 E. 58th Street, Chicago, IL 60637,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EST
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Tetrahymena thermophila.
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                                                                                                Tetrahymena thermophila
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                                            Tetrahymena thermophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: apturkew@midway.uchicago.edu
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/strain="CU428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
proc. Natl. Acad. Sci USA, 98: 8709-8713."
42 c 44 g 19 t
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44 g 18 t 1 others
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0; Mismatches
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les 16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                Unpublished (1998)
Other_ESTs: fu53f08.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 134)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Ki
,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fu53f08.yl zebrafish similar to TR:Q9Y4D4
                                                                                                          Email: zbrafish@watson.wustl.edu
cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
cDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Mashington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@genomesystems.com) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BI981973.1 GI:16371108
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920 E. 58th Street, Chicago,
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Contact: Turkewitz AP
                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniform
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                                                                                 RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Cyprinidae; Danio.
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primer: T3.
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/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in chilcoat and Turkewitz (2001)
proc. Natl. Acad. Sci USA, 98: 8709-8713."

44 c 46 g 18 t
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/strain="CU428.1"
/db_xref="taxon:5911"
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Pred. No. 64;
Mismatches
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                                                                                                                                                                                                                                                                                                                                      Email: hennig@molgen.mpg.de

5' EST sequencing of clones from a zebrafish shield stage library,

5' EST sequencing of clones from a zebrafish shield stage library,
                                                                                                                                                                                                                                                                                                                                                                                                                         Ihnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Hennig S
laboraty 123, dept.Lehrach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clark,M., Aanstad,P., Hennig,S., Johnson,S.L. and Lehrach,H. EST sequencing of a zebrafish shield stage cDNA library normalised by oligonucleotide fingerprinting Unpublished (2001)
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Danio rerio
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
Cyprindae; Danio.
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640 bp mRNA linear EST 12-OCT-2001
F637-2-000197 Zebrafish shield stage whole embryo cDNA library
MPMGp637 Danio rerio cDNA clone MPMGp637_18E17;MPMGp637E1718 5',
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                                                                                                                                                                                                                                                                                          quality sequence stop: 640.
Location/Qualifiers
  /organism="Danio rerio"
/db_xref="taxon:7955"
/clone="MPMGp637_18E17;MPMGp637E1718"
/clone=lib="Zebrafish shield stage whole embryo cDNA
/library MPMGp637"
/tissue_type="whole embryo"
/dev_stage="shield stage, 6 hrs post-fertilisation"
/dev_stage="shield stage, 6 hrs post-fertilisation"
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/note="Vector: pSportI; Site_1: NotI; Site_2: SalI;
/note="Vector: pSportI; SalI adaptors, directionally cloned,
library normalised by oligonucleotide fingerprinting"
152 c 139 g 139 t 1 others
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/note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
/note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
Original library was constructed in lambdaZIPLOX. Nexcision of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original library."
133 c 139 g 125 t
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/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Danio rerio"
/db_xref="taxon:7955"
/clone="5333151"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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Ostariophysi; Cypriniformes
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Best Local
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559 GTCGGCGAGCTGATCC 574
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                     5 gtcggcgagctgatcc 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: John Fellers

Contact: John Fellers

US Department of Agriculture, Agriculture Research Service, Plant Science and Entomology Unit

Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA
                                                                     l Similarity 100 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: jpf@alfalfa.ksu.edu
Sequence have been trimmed to remove vector
quality sequence with phred score less than
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       University, Manhattan, Tel: 785-532-2367 Fax: 785-532-6167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S. The structure and function of the expressed portion of the wheat genomes - Kansas State Unversity. Fusarium graminearum infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BE585978 708 bp mRNA linear EST 17-AUG-200 Est#7pT7_A09_a9_065 KSU wheat Fusarium graminearum infected spike cDNA library Triticum aestivum cDNA clone Est#7pT7_A09_a9_065, mRN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spike cDNA library
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Espermatophyta; Magnoliophyta; Liliopsida;
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BE585978
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                                                                                                                                                                                                                                /tissue_type="Spike"
/dev_stage="Adult plant"
/dev_stage="Adult plant"
/lab_host="E. coli JM109"
/note="Vector: pGEM-T easy; Site_1: SacII; Site_2: SpeI;
/note="Vector: pGEM-T easy; Site_1: SacII; Site_2: Spikes were sprayed
with Fusarium graminearum (at what stage). Total RNA, and
poly(A) RNA were prepared from infected spikes. CDNA was
prepared using the SmartTM PCR cDNA synthesis kit from
                                                                                                                                                                                                     Clonetech, cDNA was cloned from Promeda."
                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:4565"
/clone="Est#7p77_A09_a9_065"
/clone_lib="KSU wheat Fusarium graminearum infected spike
cDNA library"
                                                                                                                                                                                from Promega.
221 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism≈"Triticum aestivum"
/cultivar="Sumai3"
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                                                                                  80.0%;
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100.0%; Pred. No.
Live 0; Mismatc
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Pred. No.
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                                                                                                     Length 708;
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Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 237)
Altenbach, S., Anderson, O.D., Chao, S., C.C., Kang, Y., Lazo, G.R., Miller, R., Tong, J.C.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 376)
Andrews,J., Bouffard,G.G., Cheadle,C., Lu,J., Becker,K.G. and
                                                                                                                                                                        AI945868 376 bp mRNA linear EST 08-JAN-2001 b817907.yl Drosophila melanogaster adult testis library Drosophila melanogaster adult testis library Drosophila melanogaster cDNA clone bs17907 5', mRNA sequence.
AI945868 AI945868.2 GI:9991196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The structure and function of the expressed genomes - Endosperm cDNA library Unpublished (2000)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Triticae; Triticum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   quality sequence with phred score less
Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                     EST
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Sequence have been trimmed to remove vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fax: 5105595818
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                                                                                                                                    fruit fly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ECORI; Seeds collected, endosperm isolated, and RNA prepared by Susan Altenbach. Library constructed by Stratagene, Inc. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab."

3 79 c 40 g 53 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="WHE0067_F05_K09"
/clone=11b="Wheat endosperm cDNA library"
/t1ssue_type="Endosperm"
/t1ssue_type="Endosperm"
/dev_stage="5 to 30 days post anthesis seed"
/lab_host="E. coli_SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: Lambda ZAP II, excised phagemid; Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:4565"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Triticum aestivum"
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Pred. No.
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red. No. 2.3e+02;
Mismatches 0;
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Rausch,C.J.,
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., Seaton, C.L.
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Best Local
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                                                                  Eukaryota; Metazoā; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopteraygota; Diptera; Brachyeara; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 379)

Andrews, J., Bouffard, G.G., Cheadle, C., Lu, J., Becker, K.G. and Chief.
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http://www.niddk.nih.gov/intram/people/boliver.htm
http://www.niddk.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
Sequencing Center (NISC; see http://www.nisc.nih.gov).
Plate: 17 row: g column: 07
Seq primer: M13RPl reverse primer (ABI).
                                                                                                                                                                                                                                                                                                                                 AI944952 379 bp mRNA linear EST 08-JAN-200: bs07cl2.yl Drosophila melanogaster adult testis library Drosophila melanogaster cDNA clone bs07cl2 5', mRNA sequence.
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Gene discovery using transcription in the
                                                                                                                                                                                                       Drosophila melanogaster
                                                                                                                                                                                                                                                            EST
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                                                     Oliver,B.
                                                                                                                                                                                                                                 fruit fly.
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/inte_1: ECOR I; Site_2: Xho I; Testes dissected from 1-5
day adult y(*) w(67c1)/Y males raised at 25oC. RNA
isolated using Trizol (Life Technologies) and a single
round of Poly(A)+ selection using Oligotex (Qiagen). cDNA
library constructed using Stratagene ZAP-cDNA syntesis
kit. Oligo dT-primed, size fractionated -1-6 kb, and
directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
Following a single round of amplification pBlueScript SK
phagemids were mass excised. A distribution channel for
clones is being sought, but not currently available.
Requests for clones cannot be honored."

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/strain="y[*] w[67cl]/Y"
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computational and microarray analysis drosophila melanogaster testis
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Matches 15; Conservative
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Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
sequencing center (NISC; see http://www.nisc.nih.gov).
Plate: 07 row: c column: 12
Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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//dev_stage="1-5 day adult"
//lab_host="SOLR (Stratagene)"
//note="Organ: testis; Vector: pBlueScript SK (Stratagene);
Site_1: EcoR I: Site_2: Xho I: Testes dissected from 1-5
day adult y(*) w(67c1)/Y males raised at 25oC. RNA
isolated using Tritol (Life Technologies) and a single
round of Poly(A)+ selection using Oligotex (Oligen). CDNA
ilbrary constructed using Stratagene ZAP-cDNA syntesis
kit. Oligo dT-primed, size fractionated ~1-6 kb, and
directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
Following a single round of amplification pBlueScript SK
phagemids were mass excised. A distribution channel for
clones is being sought, but not currently available.
Requests for clones cannot be honored."
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/strain="y[*] w[67c1]/Y"
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/ 100.0%; Pr/
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AL483262 T. bruce1
AO783866 HS_2001_A
AL466454 T. bruce1
BH015799 BMBAC304F
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ALIGNMENTS

RESULT 1
W06754/c
LOCUS
DEFINITION REFERENCE AUTHORS TITLE JOURNAL ACCESSION VERSION KEYWORDS SOURCE COMMENT FEATURES ORGANISM source W06754 W06754.1 EST. Strigeidida; Schistosomatoidea; W06754 234 bp mRNA linear EST 01-JU SMEST0390 Schistosoma mansoni, adult worm, Gloria Franco Schistosoma mansoni cDNA clone SMPBE73 3' end, mRNA sequence. Avenida Antonio Carlos 6627, Belo Horizonte, Tel: (5531)4415611 Eukaryota; Metazoa; Platyhelminthes; Trematoda; D. etriaeidida; Schistosomatoidea; Schistosomatidae; Fax: (5531)4415409 Email: gfranco@mono Gerais Schistosoma Instituto de Ciencias Biologicas, Universidade Federal de Minas Schistosoma mansoni. [munologia primer: M13 Forward gfranco@mono.icb.ufmg Franco"

/lab_host="DH10B, JM109"

/note="Vector: BA vector; Site_1: NotI; Site_2: HindIII;

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SOURCE
ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification of new Schistosoma mansoni genes by the EST strategy using a directional cDNA library Gene 152, 141-147 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schist 1 (bases 1 to 579)
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579 bp mRNA linear EST : SMEST0325 Schistosoma mansoni, adult worm, Gloria Franco Schistosoma mansoni cDNA clone SMPBC65 3', mRNA sequence.
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//lab_host="DH10B, JM109"
//lab_host="Pector: BA vector; Site_1: NotI; Site_2: HindIII;
//lotal cellular RNA from male and female adult worms was
extracted according to a modification (Puissant, C. and
Houdebine, L. M. BioFeedback 8, 148-149, 1990) of the
cuanidine Thiocyanate procedure (Chomczynski, P. and
Sacchi, N. Anal. Biochem. 162, 156- 159, 1987). Poly (A)+
RNA was purified by oligo dT column and cDNA was
synthesized as described previously (Adams, M. D. et al.
Nature Genet. 4, 373-389, 1993). cDNA was ligated to a
                                                                                                                                                                                                                                                                                   Franco
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/clone="SMPBC65"
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                                                                                                                                                                                                                                                                                                                                                                                           /strain="NMRI"
                                                                                                                                                                                                                                                                                                       /clone_lib="Schistosoma mansoni, adult worm, Gloria
                                                                                                                                                                                                                                                                                                                                                                                                                  ∕organism≈"Schistosoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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Pred. No.
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ACCESSION VERSION

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582 GCGTTTCGATGAACCC 597

COMMENT

MEDLINE JOURNAL TITLE AUTHORS RESULT T24127/c

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5 gcgtttcgatgaaccc 20
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                                        16;
                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://imagg.llnl.gov
Plate: LLAM9761 row: m column: 03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 (bases 1 to 624)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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17; Conserv
                                                                                                                                                                                                                                                                                                                                                                      High quality sequence start: 2
High quality sequence stop: 403.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
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                                                                                                                                             /tissue_type="mmlanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo c
Average insert size 2 kb. Library constructed by Life
Technologies."
10 g 110 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            two fold molar excess of a NotI/HindIII digested plasmid DNA (lafmid BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "
                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3924266"
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100.0%; Pred. No.
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Matches 15
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Contact: McCarter JP
The Washington Univ. Nematode EST Project, 1999
Washington University School of Medicine
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108,
AW694629 452)
AW6078E03STTF1021 Developing s
NF078E03ST 5', mRNA sequence.
AW694629
AW694629.2 GI:11957636
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McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hiller, L., Kucaba, T., Thaising, B., Bowers, Y., Glibbons, M., Ritter, E., Bennett, J., Franklin, C., Tsagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    384 bp mRNA linear EST 14-NOV-201 pb21g06.yl Ancylostoma caninum L3 SS SLI TOPO vl Murphy Chiapelli McCarter Ancylostoma caninum cDNA 5', mRNA sequence.
BM077908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: est@watson.wustl.edu
The library was constructed by Claire Murphy, Brandi Chiapelli,
Dr. James McCarter at Washington University, St. Louis. DNA
Sequencing by: Washington University Genome Sequencing Center.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into pCRII-TOPO(Invitrogen) following the Topo TA cloning protocol. Nematodes were provided by Dr. Prema Arasu (Prema_Arasu@ncsu.edu) of North Carolina State University in Raleigh, NC."

1 Raleigh, NC."

2 112 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-"Vector: pCRII-TOPO (Invitrogen); Site_1: EcoRI; Site_2: EcoRI; The library was constructed by Claire Murphy, Brandi Chiapelli, and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL1 PCR based library. Ancylostoma caninum SS/L3 CNNA PCR products of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Ancylostoma caninum L3 Chiapelli McCarter"
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/db_xref="taxon:29170"
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/lab_host="DH10B"
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nes 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6 cgtttcgatgaaccc 20
              Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucel genome sequencing
project, Sanger Centre, The Wellcome Trust Genome Campus, Hinxton,
Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
nhl@sanger.ac.uk
Constructed at the Institute for Genomic Research (TIGR),
Rockville, MD. Genomic DNA isolated from a cloned population of
Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Expressed Sequence Tags from the Samuel Medicago truncatula stem library Unpublished (2000) on Apr 14, 2000 this sequence version re Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                     Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R. Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Helville, S.E., Rajandream, M.A. and Barrell, B.G.
                                                                                                                                                                                                                                                                                                Trypanosoma brucei.
Trypanosoma brucei
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Insert Length: 736 Std Error: 0.(
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Seg primer: TCACACAGGAAACAGCTATGAC
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Fax: 580 221 7380
                                                                                                                                                                                                                                                          Trypanosoma.
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/note="vector: Lambda zap; Contain
internodal stem segments"
94 c 91 g 115 t
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/db_xref="taxon:3880"
/clone="NF078E03ST"
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/tissue_type="stem"
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l Similarity 100.0%;
l5; Conservatare
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High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
                                                                                                                                                                                                                                           Seq primer: T7
Class: BAC ends
                                                                                                                                                                                                                                                                                Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2001 row: K column: 18
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1 (bases 1 to 536)
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AQ783856

HS_2001_A2_F09_T7C CIT Approved Human Genomic Sperm Library D Homo sperms genomic clone Plate=2001 Col=18 Row-K, DNA sequence.
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                     160
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                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=2001 Col=18 Row=K"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
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/db_xref="taxon:5691"
/clone="247h04"
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Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (

4 kb). The v + i method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
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Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
                                                                                                genomic survey sequence. AL477985
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="140903"
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Constructed at the Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from a cloned population of Trypanosoma brucel (TREU927/4 GUTat 10.1) was mechanically sheared to give a tight size distribution (

4 kb). The v + 1 method used for the library construction is described in detail in Smith, H. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGCGTTTCGATGAAC 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ggcgtttcgatgaac 18
                                                                                                                                                                                                                                                                                                                                      Onchocercidae; Brugia.
Onchocercidae; Brugia.
1 (bases 1 to 631)
Whitton,C., Daub,J., Ware,J., Quail,M., Hall,N., J., Guillano,D., Slatko,B. and Blaxter,M.,J., Guillano,D., Sarko,B. and blaxter,M.
                                                                                                                                      Contact: Blaxter MI Institute of Cell, Animal and Population Biology University of Edinburgh Ashworth Labs, King's Buildings, West Mains Road, 3JT, UK Tel: +44 131 650 6760 Fax: +44 131 670 5450 Email: mark.blaxter@ed.ac.uk
                                                                      Sequenced from the Brugia malayi BAC library constructed by Claire Whitton and Dr Mike Quail. The sequence was generated by The Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: nelsayed@tigr.org
Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
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                                 collaboration with Mark Blaxter, Edinburgh, UK.
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Brugia malayi
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             Seq primer:
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="190a10"
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/ 3 Brugia
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GA_Ea0002K16f Gossypium arboreum 7-10 dpa fiber library Gossypium
arboreum cDNA clone GA_Ea0002K16f, mRNA sequence.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
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15; Conserv
                                                                                                                                                                                                                                      Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
High quality sequence stop: 550.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                             Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (2000)
On Jun 8, 2000 thi
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An integrated analysis of the genetics, development, and evolution of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wing,R.A., Frisch,D., Yu,Y., Main,D:, Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
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EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                      Clemson University
100 Jordan Hall, Clemson,
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/dev_stage="microfilaria (L1)"
/note="Vector: pBACe3.6; Site_1: BamH I; Brugia malayi
/note="Vector: pBACe3.6; Site_1: BamH I; Brugia malayi
genomic DNA was partially cleaved with Sau3A I and size
fractionated. 7,392 clones were generated with mean insert
size -48 kbp. The library was constructed by Claire
whitton, Blaxter Nematode Genetics Lab, University of
Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
Unit, The Sanger Centre, Cambridge, UK."
/clone="GA__Ea0002K16f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
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/strain="TRS"
/db_xref="taxon:6279"
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                                                                                                                                        /db_xref="taxon:29729"
                                                                                                                                                               /cultivar="8400"
                                                                                                                                                                                     /strain="AKA"
                                                                                                                                                                                                    /organism="Gossypium arboreum"
                                        ab_host="E. coli"
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Tetraodon
073004 of
mRNA sequence.
BM007170
                         BM007170
603614933T1 NIH_MGC_110
                                                                                                                                                                                                                                                                                                                                                                    Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
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15; Conserv
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Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human gene number estimate provided by genome wide analysis using Tetraodon nigroviridis DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genoscope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Charaterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Roest-Crollius, H., Jaillon, O., Dasilva, C., Fizames, C., Fisher, C., Bouneau, L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tetraodontidae; Tetraodon.

1 (bases 1 to 1033)
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                                                                                                                                                                                                                                                            /Clone_lib="G"
/note="Genoscope sequence ID :
/note="Genoscope sequence ID :
222 c 276 g 261 t
                                                                                                                                                                                                                                                                                                             /organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="073004"
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100.0%;
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Pred. No.
                       1218 bp mF
Homo sapiens
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                                                                                                                                                                                          DB 44;
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42;
                                          mRNA
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                         RNA linear EST 30-OCT-2001 CDNA clone IMAGE:5420816 3',
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VERSION
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                                                                            DNA Res.
20539644
                                                                                                Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Nakamura, Y. and Tabata, S.

Generation of expressed sequence tags from low-CO2 and adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
                                                                                                                                                                                                                                                                                   Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Chlorophyta; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                              AV640031 247 bp mRNA linear EST AV640031 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas cDNA clone HCL009b04_r 5', mRNA sequence.

AV640031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can inform through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1876 row: a column: 09
High quality sequence start: 25
High quality sequence stop: 313.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                   EST
                                                Contact: Erika Asamizu
                                                                                                                                                                                                                                        Chlamydomonadaceae; Chlamydomonas. 1 (bases 1 to 247)
                   The First Laboratory for Plant Gene Research
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Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mammalia; Eutheria; Primates; Co
1 (bases 1 to 1218)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, N
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/clone_tib="NIH_MGC_110"
/tissue_type="ductal carcinoma, cell line"
/lab host="DHIOB (phage-resistant)"
/note="Organ: pancreas; vector: pOTB7; Site_1: xhoI;
/site_2: EcoRI; colA made by oligo-dT priming.
Site_2: EcoRI; colA made by oligo-dT priming.

Site_2: EcoRI; colA made by oligo-dT pithing the
following 5' adaptor: GGCACCAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).

Note: this is a NIH_MGC Library."

70 a 446 c 244 g 154 t 4 others
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DNA Research Institute
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/db_xref="taxon:9606"
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                                                                          Query Match 70.0%; Score 14; DB 9; L Best Local Similarity 100.0%; Pred. No. 1.5e+02; Matches 14; Conservative 0; Mismatches 0;
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Best Local Similarity
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4 ggcgtttcgatgaa 17
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254 GGCGTTTCGATGAA 241
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                                                                                                                                                                                                                                                                                                                                                                                      Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 269)
Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K., Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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AV640876 AV640876 GI:10784204
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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                                                                                                                                                                                          /organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="haxon:3055"
/clone="HCL024a01_r"
/clone=lib="Chlamydomonas reinhardtii 5% CO2"
/clone=lib="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
dloxide"
a 85 c 60 g 59 t
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
/note: The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
dioxide"
a 79 c 54 g 53 t
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/clone="HCL009b04_r"
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/organism="Chlamydomonas reinhardtii"
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100.0%; Pr
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                                                                                                              Length 269;
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Search completed: August 7, 2002, 23:12:33 Job time: 11072 sec

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Gapop 60.0 , Gapext 60.0
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Copyright (c) 1993 - 2000 Compugen Ltd
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and is derived Pred. No. is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.

SUMMARIES

0000000 987654 W 2 P	Result
222222222 000000000	Score
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20 21 20 21 432 14 480 21 620 17 620 17 620 17 970 17 970 17 970 22	ength I
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AAA49824 AAA49826 AAQ61457 AAA49863 AAT29126 AAT29124 AAT29125 AAT29175 AAT09676	ĬĎ
Mycobacterium tube Mycobacterium tube Mycobacterium tube Mycobacterium tube rpoB gene fragment mycobacterium tube	Description

C 444 5	40 41 c 42	c c c 38	C 35	c 31 33	29 30	26 27 28	223 24 25	18 20 21	c 15 c 15 c 16	c 10 c 11 c 12
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AAZ38124 AAS94186 ABL26802	AAF89013 AAS92952 AAS92789	AAH53127 AAC48699 AAC32775	ABL22843 AAV74720 AAH68314	AAF71326 AAF27618 AAS87269	AAV04619 AAC90901	AAV04618 AAC90900 AAS94185	ABL18446 AAF61643 AAT13651 AAF61568	ABL32551 ABL18447 AAX13246 ABL33903	AAT19670 AAQ51532 AAS51357 AAS52892	AAH02079 AAA74651 AAA89994 AAT12096
Human FATP variant DNA encoding novel Drosophila melanog	Murine FATP1 codin DNA encoding novel DNA encoding novel	S. epidermidis ope Arabidopsis thalla Arabidopsis thalla	Drosophila melanog Staphylococcus aur C glutamicum codin	m -	യയ	Flea aminopeptidas Flea aminopeptidas DNA encoding novel	Drosophila melanog Lactobacillus case ACNPV ORF 43, resi Lactobacillus case	Human immune syste Drosophila melanog Enterococcus faeca Human immune syste	cobacterium leprae rpoE terococcus terococcus	Mycobacterium tube Mycobacterium tube M. tuberculosis rp

ALIGNMENTS

AAA49824 RESULT AAA49824; AAA49824 standard; DNA; . __ 20 BP.

25-SEP-2000

(first entry)

Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer; Mycobacterium tuberculosis rpoB gene amplification primer rpoB-R.

Mycobacterium tuberculosis.

WO200036142-A1.

22-JUN-2000

10-DEC-1999; 99WO-CA01177.

11-DEC-1998; 98US-0111794.

(VISI-) VISIBLE GENETICS INC

Shipman R;

WPI; 2000-431611/37.

Method for the detection and characterization of Mycobacterium tuberculosis with antibiotic resistance in a sample $\boldsymbol{\cdot}$

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AAA49826
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Best Local :
The present sequence is that of the Mycobacterium tuberculosis
                                                                            Method for the detection and tuberculosis with antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of the rpoB gene (see AAA4983). Amplification and cycle sequence primers (see AAA49823-62) have been developed for the detection are analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphc pr (isoniazid), mabA (isoniazid), rpsL/sl2 (streptomycin), 165/rrs (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA (ciprofioxacin) and 23S (azithromycin) genes of M. tuberculosis. These primers can be used in a method for the detection and
                                         Claim 4; Page 5; 43pp; English.
                                                                                                                                                                               Shipman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-3s
                                                                                                                                          WPI; 2000-431611/37.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         characterization of M. tuberculosis present in a sputum sample. The method involves performing a sequencing procedure, with or without prior amplification, to detect the presence of M. tuberculosis, and if present to evaluate the rposh, katG, rpsi/s12 and 23S genes for the presence of antibiotic inducing mutations. If M. tuberculosis is detected, a second sequencing procedure is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     performed on the sample to evaluate additional genes for the presence of antibiotic resistance-inducing mutations. Genotypic tests are rapid, sensitive and acceptance.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      resistance; rpoB gene; rifampin resistance; primer;
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                                                                                                                                                                                                                      GENETICS INC
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                                                                              characterization resistance in a s
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30-APR-1992;
14-AUG-1992;
                      WPI; 1993-368812/46
                                                                                                              (MEDI-)
            P-PSDB; AAR51372
                                                            Bodmer T,
                                                                                                                         (ASSI-) ASSISTANCE PUBLIQUE (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                    M.tuberculosis rpoB gene fragment.
                                                                                                                                                               16-APR-1993;
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                                                                                                                                                                                                                                                                                                         Mycobacterium
                                                                                                                                                                                                                                                                                                                                  mutant;
                                                                                                                                                                                                                                                                                                                                             rifampicin;
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MEDICAL RES COUNCIL.
UNIV BERNE.
UNIV CURIE PARIS VI P & M.
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20; Conser
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                                               Zhang
                                                           Cole
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                                                                                                                                                             92FR-0011098.
92US-0875940.
92US-0929206.
93FR-0004545.
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RESULT 4
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Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCR amplification was used to obtain rpoB genes iron with the resistant Mycobacterium leprae strains. A comparison with the sequence of the rpoB gene from sensitive strains (AAQ51532) revealed mutations in the region encoding amino acids 400-450. The corresp.

----ion was isolated from M tuberculosis (AAQ61457). A common
                                                                                                                                WPI;
         rpoB (rifampin resistance) gene (bp2161-2640). Amplification and cycle sequencing primers (see AAA9923-62) are used for the detection and analysis of antiblotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium
                                                                         Disclosure; Page 5; 43pp;
                                                                                                tuberculosis
                                                                                                          Method
                                                                                                                                                                                               11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                            Antibiotic resistance; rpoB
                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis rpoB gene (rifampin resistance).
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                                                                                                                                                                        (VISI-) VISIBLE GENETICS INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isoniazid, rifampicin or strep
by detecting mutation in katG,
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                                                                                                                                2000-431611/37.
                                                                                              for the detection and characterizulosis with antibiotic resistance
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                                                sequence is that of the Mycobacterium tuberculosis
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 mabA (isoniazid),
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372..391
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                                                                                                         characterization of Mycobacterium
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(streptomycin),
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RESULT 5
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09-NOV-1994;
09-MAR-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis. These primers can be used in a method for the detection and characterization of M. tuberculosis present in a sputum sample. The method involves performing a sequencing procedure, with or without prior amplification, to detect the presence of M. tuberculosis, and if present to evaluate the rpoB, katG, rpsL/Sl and 23S genes for the presence of a second sequencing procedure is If M. tuberculosis is detected, a second sequencing procedure is performed on the sample to evaluate additional genes for the
                       Cleavage of nucleic acids using an enzyme, especially a nuclease selected from the group consisting of Cleavase (RTM) BN enzyme, Thermus aquaticus DNA polymerase, Thermus thermophilus DNA polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae Radi/Radio complex. The nucleic acid substrate is preferably an
                                                                                                                                                                            WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                             p53; mutant; mutation; cleavage; nuclease; cleavase; Escherichia; Saccharomyces; Campylobacter; Mycobacte Staphylococcus; identification; detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       presence of antibiotic resistance-inducing mutations. tests are rapid, sensitive and accurate providing infantibiotic treatment options.
               oligonucleotide
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                                                                                                                                                                                                   Oldenburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT29126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAT29126 standard;
                                                                                                   Example
                                                                                                                                                                                                               Brow MAD,
                                                                                                                                                                                                                                       (THIR-) THIRD
                                                                                                                                                                                                                                                                                                                              09-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                     23-MAY-1996
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                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TACGGCGTTTCGATGAACCC
                                                                                                                                                                            1996-259862/26
                                                                                                   33;
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numan p53 gene, to
                                                                                                                                                                                                  Dahlberg
MC, Olive
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                                                                                                 Page 306; 433pp; English
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94US-0337164.
95US-0402601.
95US-0484956.
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            containing
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a human p53 gene sequence
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RESULT 6
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DE rpoB gene fragment f
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PR 09-MAR-1995; 95US
PR 07-JUN-1995; 95US
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       Cleavage of nucleic acids using an enzyme, especially a nuclease selected from the group consisting of Cleavase (RTM) BN enzyme, Thermus aquaticus DNA polymerase, Thermus thermophilus DNA polymerase, Escherichia coli ExoIII and the Saccharomyces cerevis Radl/Radl0 complex. The nucleic acid substrate is preferably an oligonucleotide containing a human p53 gene sequence or alternatively, microbial gene sequences. Cleavage products are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 compared to the cleavage products of reference gene sequences. The method is used for detecting mutation in the human p53 gene; for identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The method may also be used for the identification of viruses, especially hepatitis C virus (HCV) and similar immunodeficiency virus (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bg region of the Mycobacterium tuberculosis rpoB gene, which, when mutated is associated with rifampin resistance. The 620 bg region amplified spans both the H451Y and S456L mutations. The amplified fragments are given in AAT29124 (Wild type) and AAT29125-26
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human p53 gene,
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94US-0337164.
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        Cleavage of nucleic acids using an enzyme, especially a nucleat selected from the group consisting of Cleavase (RTM) BN enzyme Thermus aquaticus DNA polymerase, Thermus thermophilus DNA polymerase, Thermus thermophilus BNA polymerase, Scherichia coli ExoIII and the Saccharromyces care Radl/RadlO complex. The nucleic acid substrate is preferably oligonuclectide containing a human p53 gene sequence or
 alternatively,
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                                                                                                                                                                                                                                                                                                                                                                                                                         p53; mutant;
Escherichia;
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an p53 gene,
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Saccharomyces; Campylobacter;
us; identification; detection;
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95US-0402601.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
products
                                                        y a nuclease
BN enzyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 620;
                                    cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                       Shigella;
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RESULT
AAT09676/
ID AAT0
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The method may also be used for the identification of viruses, especially hepatitis C virus (HCV) and simian immunodeficiency virus (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp region of the Mycobacterium tuberculosis rpoB gene, which, when mutated is associated with rifampin resistance. The 620 bp region amplified spans both the H451Y and S456L mutations. The amplified fragments are given in AAT29124 (Wild type) and AAT29125-26
misc_feature
                              misc_feature
                                                            misc_feature
                                                                                                                                                                                                                                                                                                                 primer_bind
                                                                                                                                                                                                                                                                                                                                                 Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                   polymerase
                                                                                                                                                                                                                                                                                                                                                                              Tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium
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)676/c
AAT09676 standard;
                                                                                           misc_feature
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                                                                                                                                                                                                                                                                                                                            Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT09676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 620 BP; 103 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               compared to the cleavage products of reference gene sequences. 'method is used for detecting mutation in the human p53 gene; for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutant sequences).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 tacggcgtttcgatgaaccc
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                   chain reaction;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                  disease diagnosis; oligonucleotide; DNA primer;
ain reaction; DNA amplification; rpoB locus; TB;
                                                                                                                                                                                                                                                                                                                                                 tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis rpoB
                                                                                 /note= "M.
433..434
/*tar=
                              /note= "N
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438
/*tag=
/note=
486
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/note= "primer KY290"
372..373_
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226..240
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                                                                                                                                                                                       /note= "primer
348..373
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                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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226..243
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          tuberculosis
                                        tuberculosis
                                                                      tuberculosis signature
                                                                                                   tuberculosis signature nucleotide'
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                                                                                                                                                                                              rpo95"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214
                                                                                                                                                                rpo105
                                                                                                                                                                                                                                                                                                                                                                                                gene DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 17;
0.0073;
          signature
                                        signature
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          nucleotide'
                                         nucleotide'
                                                                      nucleotide'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                                                                                                                   PCR;
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β Q

671

tacggcgtttcgatgaaccc

20

0;

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Query Match
Best Local S
Matches 20
                                                             This oligonucleotide DNA primer is specific for Mycobacterium tuberculosis, and may be used to amplify a sample DNA by targeting a portion of the gene encoding rpoB. The lst several bases comprise nonhybridizing tail consisting of filler bases followed by a restriction site incorporated to facilitate cloning using the amplicon at a later date, if desired. The remaining bases hybridize to bacterial rpoB DNA. The method provides for the detection of M. tuberculosis and the concurrent determination of its drug susceptibility, particularly to rifamycin. The method can provide often greater than 95% sensitivity and 100% specificity. The biological sample is a fluid or tissue sample from a human.
                                                                                                                                                                                                 Detection of Mycobacterium tuberculosis - \ensuremath{\mathbf{w}} ith a primer set that targets portions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                Disclosure; Fig.3; 54pp;
                                                                                                                                                                                                                               WPI; 1996-030581/03
                                                                                                                                                                                                                                                                                                                                                07-DEC-1995
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                                              Sequence
                                                                                                                                                                                                                                                 Young
                                                                                                                                                                                                                                                           Felmlee TA,
                                                                                                                                                                                                                                                                             (HOFF ) HOFFMANN LA ROCHE INC (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                          26-MAY-1994;
                                                                                                                                                                                                                                                                                                                             26-MAY-1995;
        Similarity
                                              970 BP; 182 A; 302 C;
Conservative
                                                                                                                                                                                                                                                           Hunt JM,
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952..966
/*tar-
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525
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952..966
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525..541
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516
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501
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       100.0%;
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                                                                                                                                                                                 English.
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0;
        Score
Pred.
                                              330 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           rpo397"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rpo273"
                                                                                                                                                                                                                                                                                                                                                                                                                 NMQRQ-1"
Mismatches
         NO;
                                                                                                                                                                                                                                                            Roberts
                                              156
    , DB 17;
0.0071;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                signature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    signature
                                              T; 0 other;
                                                                                                                                                                                                   by amplifying sample DNA f the gene encoding rpoB.
                                                                                                                                                                                                                                                           9
0;
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                 Length 970;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                nucleotide"
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Indels
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Gaps
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ID AAH02079
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AAH51976/c
                                                                                                                                                             Query Match
Best Local S
Matches 20
                                                                                                                                                                                                                                                          This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polypucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of peptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of an organism.
                                                                                                              1529 TACGGCGTTTCGATGAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 68-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eisenberg
24-JUL-2001
                         AAH02079;
                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-NOV-1999;
01-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1999;
                                                                                                                                                               Local Similarity
nes 20; Conserv
                                                                         10
                                                                                                                           1 tacggcgtttcgatgaaccc 20
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DB; AAG81125.
                                                  standard;
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                                                                                                                                                                Conservative
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(first entry)
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                                                                                                                                                                                                                             BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99US-0165086
99US-0165124
                                                                                                                                                                                                                             675
                                                  DNA;
                                                                                                                                                                           100.0%;
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                                                  3534
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                                                                                                                                                                           Score 20; I
Pred. No. 0.
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                                                                                                                                                               Mismatches
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                                                                                                                                                                         DB 22;
0.0064;
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                                                                                                                                                                0
                                                                                                                                                                                      Length 3519;
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                                                                                                                                                                                                                           other;
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                                                                                                                                                             0;
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Вр
                                                                                                                                                                                       CC nucleic acids of the first fus, amb and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical cc species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more crelated microorganisms e.g. algae, archaea, bacteria, fungal and correct contact and information and identification of an algal, archaeal, bacterial, fungal and correction and identification of an algal, archaeal, bacterial, fungal cc and parasitical species, genus, family and group. A nucleic acid (I) cobtained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the ce detection of any bacterium, fungus or parasite in a sample and for the last one toxin gene. hexa nucleic acids are used for the specific and uniquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against cmicroorganisms. Microbalal species or genus or family or phylum or group corresponded to the species of genus or family or phylum or group corresponded to the species and staphylococcus sp. Streptococcus sp., which can be detected include Abiotrophia addacens, Bordetella sp., corresponded in an hour and improved accuracy is also achieved.

CC Mah00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
                                                                          Matches
                                                                                         Query Match
Best Local :
 1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    microorganism; diagnosis; translation elongation factor Tu; to translation elongation factor G; RecA recombinase; resistance; catalytic subunit of proton-translocating ATPase; antimicrobia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of archaeal, bacterial, fungal and parasitical species in a test same
                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Picard FJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-SEP-1999; 99CA-2283458
19-MAY-2000; 2000CA-2307010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identification;
                                  1 tacggcgtttcgatgaaccc
TACGCCGTTTCGATGAACCC
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                                                                          20;
                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           specific;
                                                                                                                                                                  3534 BP;
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                                                                      Conservative
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; algal; a
                                                                                                                                                                679 A; 1081 C;
                                                                                       100.0%;
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archaeal; bacterial;
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 1528
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                                                                                       Score 20;
Pred. No.
                                                                          Mismatches
                                                                                                                                                                1188 G;
                                                                                         0.0064;
                                                                                                           DB 22;
                                                                                                                                                                586 T;
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                                                                                                                                                                  0 other;
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                                                                                                       Length 3534;
                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           detection;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of algal,
sample -
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                                                                      Gaps
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RESULT 12
AAA89994/c
ID AAA899
XX AAA899
AC AAA899
XX 18-DEC
XX M. tub
XX Drug r
KW Drug r
KW RNA po
XX Mycoba
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAA74651/c
ID AAA74651 standard;
                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                         Rifampin resistance is largely associated with point mutations localised in a small core region of 81 base pairs in the rpoB gene, which encodes the RNA polymerase beta subunit. To detect a mutation, a complex is formed comprising a first sequence representing the predetermined region of the gene of the organism and a second sequence representing the corresponding region of the gene of the wild type organism in double stranded form. Each member of at least one pair of non-complementary stranded form. Each member of at least one pair of non-complementary stranded within the complex has a label. The association of the labels in the complex is related to the presence of the mutation. The presence of
                                                                                                                                                                                                                                           2122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is the rooB gene from Mycobacterium tuberculosis. Rifampin resistance is largely associated with point mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-2000
                 Mycobacterium tuberculosis
                                           RNA polymerase beta subunit;
                                                       Drug resistance; rifampin; rifampicin;
                                                                                                                18-DEC-2000
                                                                                                                                            AAA89994;
                                                                                                                                                                      AAA89994 standard;
                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 1; Fig 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method for detecting drug resistance in a strain of an organism, particularly for detecting rifampin resistance in Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-524243/47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200043546-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu YP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (DADE-) DADE BEHRING INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rifampin resistance; mutation detection;
                                                                                                                                                                                                                                                                                                Local Similarity 100 nes 20; Conservative
                                                                                                                                                                                                                                                          1 tacggcgtttcgatgaaccc 20
                                                                                                                                                                                                                                                                                                                                                                                             mutation is related to the drug resistance of the strain.
                                                                                                                                                                                                                                           TACGGCGTTTCGATGAACCC 2103
                                                                                                                                                                                                                                                                                                                                                                    3853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Kurn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                    BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tuberculosis rpoB gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0233996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99WO-US30377
                                                                                   rpoB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86pp;
                                                                                                                                                                                                                                                                                                                                                                   723 A; 1173 C;
                                                                                                                                                                      DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA; 3853
                                                                                   gene encoding RNA
                                                                                                                                                                                                                                                                                                           100.
                                                                                                                                                                      3853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English.
                                                                                                                                                                                                                                                                                                              09:
                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            rpoB; RNA polymerase beta subunit;
                                           ds.
                                                                                                                                                                      ВÞ
                                                                                                                                                                                                                                                                                              Score 20; DB Pred. No. 0.0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                    1293 G;
                                                                                 polymerase beta subunit.
                                                       pyrazinamide;
                                                                                                                                                                                                                                                                                                DB 21;
0.0064;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                  664 T;
                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                          Length 3853;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a method for detecting drug resistance in a strain of an organism. The method comprises detecting the presence of a least 1 mutation in a first sequence and relating the presence of the mutation to drug resistance. Included in the invention are a kit for carrying out the method and a method for detecting the presence of a difference between two related nucleic acid sequences in an organism. I methods are useful for detecting resistance to drugs such rifampin and pyrazinamide in Mycobacterium. The present sequence represents the Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase beta subunit). The sequence is used in an example of the method of the invention for the detection of rifampin resistance in M. tuberculosis.
                                                                                                                                                                                        Antibiotic; resistance; spectrum; gene; mycobacterium; determination; amplification; tuberculosis; rpoB; frag primer; differential; hybridisation; pattern; rifampic
                                                                                                                                                                                                                                                                                                                                                                                        2122 TACGGCGTTTCGATGAACCC 2103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3853 BP; 723 A; 1173 C; 1293 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Detecting resistance of drugs such as rifampicin in strains \mbox{\it Mycobacterium}, comprising detecting mutations in a gene and them to drug resistance -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-499235/44
                                                 09-JUN-1994;
                                                                                                                             WO9533851-A2
                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                        10-JUL-1996
                                                                                                                                                                                                                                                                                                                        AAT12096 standard;
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                        (INNO-) INNOGENETICS NV
                                                                          09-JUN-1995;
                                                                                                     14-DEC-1995
                                                                                                                                                                                                                                             M. tuberculosis rpoB gene fragment amplification
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22-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                      (first entry)
                                                 94EP-0870093
                                                                           95WO-EP02230
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99US-0296894
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                                                                                                                                                                                                                                                                                                                          DNA;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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                                                                                                                                                                                                                                             primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 3853;
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                                                                                                                                                                                                       fragment;
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Machtelinckx L,

Portaels

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RESULT 1
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ID AATO9670
XX AATO
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KW Poly
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OS Synt
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PA (H01
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PI Y00
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Best Local S
Matches 19
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This oligonucleotide DNA primer is specific for Mycobacterium tuberculosis, and may be used to amplify a sample DNA by target a portion of the gene encoding rpoB. The method provides for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The antibiotic resistance spectrum (ARS) of a mycobacterium of determined by amplifying the relevant part of the antibiotic resistance gene, i.e. the M. tuberculosis rpoB gene fragment amplified using the primer set AAT12091-98, hybridising it will least 1 rpoB gene probe, detecting the hybrids formed and inferring the ARS, and opt. the spp., from the differential hybridisation patterns. The method is partic, useful for the
                                                                                                                                                                                                                                                Felmlee TA,
Young KKY;
                                                                                                                                                                                                                                                                                                                (HOFF )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      07-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection of rifampicin and/or rifabutin resistance in M. leprae or M. tuberculosis, and mycobacterial spp. identification. The method is rapid and reliable and provides simultaneous determn.
                                                                                             Claim
                                                                                                                                        with a
                                                                                                                                                            Detection of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                  26-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                           26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09533074-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT09670;
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                                                                                                                                        primer
                                                                                                                                                                                                                                                                                                                HOFFMANN LA ROCHE INC MAYO FOUNDATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19
                                                                                             Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        d primers for determn. of antibiotic resistance spectrum rlum, opt. coupled with species identification - from patterns of hybridisation with rpoB gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   spp. identity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chain
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ilarity 100.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BP;
                                                                                                                                                                                                                                                                       Hunt
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                                                                                                                                        set
                                                                                             39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 disease diagnosis; oligonucleotide; DNA primer;
ain reaction; DNA amplification; rpoB locus; TB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                9405-0250030.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 A;
                                                                                                                                      that targets portions
                                                                                             54 pp;
                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 C;
                                                                                                                                                                                                                                                                     Persing
                                                                                             English
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                                                                                                                                                                                                                                                                       Roberts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 17;
0.038;
                                                                                                                                                               bγ
                                                                                                                                   by amplifying sample DNA the gene encoding rpoB.
                                                                                                                                                                                                                                                                   GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                     Whelen
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    targeting s for the
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RESULT 15
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Best Loc
Matches
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30-APR-1992;
14-AUG-1992;
16-APR-1993;
                                                                                            WPI; 199
P-PSDB;
PCR amplification was used to obtain rpoB genes from rifamplcin-
resistant Mycobacterium leprae strains. A comparison with the
sequence of the rpoB gene from sensitive strains (AAQS1532) revea
mutations in the region encoding amino acids 400-450. A common
                                                      Rapid detection of antibiotic resistance in Mycobacteria isoniazid, rifampicin or streptomycin resistance in tube by detecting mutation in katG, rpoB or rpsL genes
                                                                                                                                                                                                                                                                                                                                   CDS
                                                                                                                   Young
                                                                                                                                                    (INSP)
                                                                                                                                                                              (ASSI-)
                                                                                                                                                                                                                                                                                                                                                          Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                           mutant;
                                                                                                                                                                                                                                                                                                                                                                                                   M.leprae rpoB
                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ51532
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       detection of M. tuberculosis and the concurrent determination drug susceptibility, particularly to rifamyclin. The method caprovide often greater than 95% sensitivity and 100% specificit The biological sample is a fluid or tissue sample from a human
                                          Example
                                                                                                                                                                                                                                        30-APR-1993;
                                                                                                                                                                                                                                                        11-NOV-1993.
                                                                                                                                                                                                                                                                         WO9322454-A.
                                                                                                                                                                                                                                                                                                                                                                                   rifampicin;
                                                                                                                                                                                                                                                                                                                                                                                                                    17-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAQ51532;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ш
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               6
                                                                                            1993-368812/46.
DB; AAR43671.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cgtttcgatgaaccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cgtttcgatgaaccc
                                                                                                                   Á
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15; Conservative
                                                                                                                                                     VIND
                                          <u>۷</u>
                                                                                                                                             UNIV CURIE
                                                                                                                                                             MEDICAL RES
                                                                                                                                                                            ASSISTANCE PUBLIQUE
                                                                                                                                                                       INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                      standard; DNA;
                                                                                                                   Cole
Zhang
                                         Fig
                                                                                                                                                                                                                                                                                                                                                                                   antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP;
                                                                                                                                                     BERNE
                                                                                                                                                                      PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                  gene
                                                                                                                                                                                              92FR-0011098.
92US-0875940.
92US-0929206.
93FR-0004545.
                                                                                                                                                                                                                                                                                                                                                           leprae
                                          12;
                                                                                                                                                                                                                                        93WO-EP01063
                                                                                                                    Υ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        σ
                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1..3447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Α;
                                        97pp;
                                                                                                                                            PARIS VI
                                                                                                                           Неут
                                                                                                                                                             COUNCIL
                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15
                                                                                                                                                                                                                                                                                              "rifampicin-sensitive;
strains the Ser codon
nucleotides 1273-1275)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     3447
                                                                                                                                                                                                                                                                                         ç
                                                                                                                                                                                                                                                                                                                                                                                  susceptibility;
                                                                                                                           ₿,
                                          English
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ი
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                                                                                                                                                                                                                                                                                        Phe, Met or esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score :
                                                                                                                            Honore
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 T;
                                                                                                                                             ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15;
No.
                                                                                                                           ž
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1
                                                                                                                           Telenti
                                                                                                                                                                                                                                                                                                                                                                                   sensitive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                                                                                        (TCG
                                                                                                                                                                                                                                                                                        ) is often mutated 
Leu codon"
                                                                                                                                                                                                                                                                                                                  in resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                           A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                  in tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                   resistant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               specificity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 its
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CC mutation seen in resistant strains occurs at codon 425 where Ser is CX substituted, most frequently by Leu.

XX Squence 3447 BP; 687 A; 965 C; 1139 G; 656 T; 0 other;

Query Match
Best Local Similarity 100.0%; Score 14; DB 14; Length 3447;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 14; Conservative 0; Mismatches 0; Indeis 0; Gaps 0;

Qy 7 gittcgatgaaccc 20
Db 1448 GTTTCGATGAACCC 1435

Search completed: August 8, 2002, 00:01:22

Job time: 7611 sec
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RESULT 6
AAT29124/c
ID AAT29124 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  compared to the cleavage products of reference gene sequences. The method is used for detecting mutation in the human p53 gene; for identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigeila and Staphylococcus. The method may also be used for the identification of viruses, especially hepatitis C virus (HCV) and similar immunodeficiency virus (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp region of the Mycobacterium tuberculosis rpoB gene, which, when mutated is associated with rifempin resistance. The 620 bp region amplified spans both the H451Y and S456L mutations. The amplified fragments are given in AAT29124 (Wild type) and AAT29125-26
                                                                                                                                                                                                                                                                                                                                                  Brow MAD,
Oldenburg
                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-AUG-1995;
09-NOV-1994;
09-MAR-1995;
07-JUN-1995;
Cleavage v. .... Cleavage v. .... Cleavage v. .... Selected from the group consisting v. .... hermophilus DNA polymerase, Thermus thermophilus DNA Polymerase, Thermus the Saccharomyces cerevisiae polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae polymerase, Escherichia and Saccharomyces or Saccharomyces cerevisiae polymerase, Sacchar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 620 BP;
                                                                                                                                                                                                                                               esp.
                                                                                                                        Cleavage of nuclei
selected from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p53; mutant;
Escherichia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (mutant sequences).
                                                                                                                                                                                                                                                                   Cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9615267-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rpoB
                                                                                                                                                                                     Example 33; Page
                                                                                                                                                                                                                                                                                                                                                                                                                   (THIR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene fragment from Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TACGGCGTTTCGATGAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tacggcgtttcgatgaaccc
                                                                                                                                                                                                                                                                                                                1996-259862/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     THIRD
                                                                                                                                                                                                                                                 human
                                                                                                                                                                                                                                                                       of nucleic
                                                                                                                                                                                                                                                                                                                                                     Ų
Ķ
                                                                                                                                                                                                                                                                                                                                                                        Dahlberg
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                                                                                                                                          nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mutation; cleavage; nuclease;
Saccharomyces; Campylobacter;
us; identification; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                   WAVE TECHNOLOGIES INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                          95US-0520946.
94US-0337164.
95US-0402601.
95US-0484956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tuberculosis
                                                                                                                                                                                                                                               p53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95WO-US14673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     103
                                                                                                                                                                                     305; 433pp;
                                                                                                                                                                                                                                               gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DNA;
                                                                                                                                                                                                                                                 acids tene, to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                                                                                                                                                                                                                                                                                                                                                         DM;
                                                                                                                        acids using an roup consisting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  277
                                                                                                                                                                                                                                                 to detect mutation(s) - identify strains of mid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ü
                                                                                                                                                                                     English.
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Pred.
                                                                                                                                                                                                                                                                                                                                                                            Ĺ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                     n enzyme, especially a nuc
g of Cleavase (RTM) BN en:
Thermus thermophilus DNA
                                                                                                                                                                                                                                                                                                                                                                          Heisler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G
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No.;
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                                                                                                                                                                                                                                                                                                                                                                            Ĭ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cleavase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium; Shigella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                   microorganisms and
                                                                                                                                                                                                                                                                                                                                                                            Lyamichev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                         allows detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thermus;
                                                                                                                        nuclease
enzyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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RESULT
AAT29125/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The method may also be used for the identification of viruses, especially hepatitis C virus (HCV) and simian immunodeficiency virus (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp region of the Mycobacterium tuberculosis rpoB gene, which, when mutated is associated with rifampin resistance. The 620 bp region amplified spans both the H451Y and S456L mutations. The amplified fragments are given in AAT29124 (Wild type) and AAT29125-26
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AAT29125
                                                                                                                      Cleavage
esp. in h
                                                                                                                                                                                                                                    30-AUG-1995;
09-NOV-1994;
09-MAR-1995;
07-JUN-1995;
                                                                                                                                                                                       Brow
                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT29125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               compared
                                                                                                                                                                                                                                                                                                                                         W09615267-A1
                                                                                                                                                                                                                                                                                                                                                              Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                              p53; mutant;
Escherichia;
                                                                                                                                                                                                                                                                                                                                                                                                                              rроВ gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-1996
                              selected from the group consisting of Cleavase (RTM) BN en Thermus aquaticus DNA polymerase. Thermus thermophilus DNA polymerase, Escherichia coli ExoIII and the Saccharomyces
                                                                                                                                                                              Oldenburg
                                                                                                                                                                                                                                                                                             09-NOV-1995;
                                                                                                                                                                                                                                                                                                                  23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (mutant sequences).
                                                                 Cleavage
                                                                                      Example
                      Rad1/Rad10 complex. The nucleic acid substrate is preferably
                                                                                                                                                                                                               (THIR-) THIRD WAVE TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 tacggcgtttcgatgaaccc
                                                                                                                                                                                        MAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACGGCGTTTCGATGAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ed to the cleavage products of reference gene sequences. The is used for detecting mutation in the human p53 gene; for fying strains of microorganisms, especially bacteria selected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                       33;
                                                                                                                       numan
                                                                                                                                   0f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  standard; DNA;
                                                                of nucleic acids using
                                                                                                                                                                                                                                                                                                                                                                                                                              fragment (mutant) from
                                                                                                                                                                              ЖĊ,
                                                                                                                                                                                          Dahlberg
                                                                                                                                   nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ВP;
                                                                                       Page
                                                                                                                                                                                                                                                                                                                                                                                    mutation; cleavage; nuclease;
Saccharomyces; Campylobacter;
us; identification; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                               Olive
                                                                                                                                                                                                                                    95US-0520946.
94US-0337164.
95US-0402601.
95US-0484956.
                                                                                                                                                                                                                                                                                                                                                              tuberculosis
                                                                                                                                                                                                                                                                                             95WO-US14673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         103 A;
                                                                                       305-306;
                                                                                                                       gene,
                                                                                                                        ene, to
                                                                                                                                                                               JE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  620
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .0%;
                                                                                                                                                                                           Fors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        277
                                                                                      433pp;
                                                                                                                                   ç
                                                                                                                       co detect mutation(s) identify strains of a
           a human p53 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20; DE Pred. No. 0.0
                                                                                                                                                                                          Ļ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          214
                                                                an
                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis.
                                                                                       English.
                                                                                                                                                                                            Heisler
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و
                                                     enzyme, especially of Cleavase (RTM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           T; 0
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                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                          cleavase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other;
                                                                                                                        microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 620;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                         BN BN
                                                       enzyme,
                                                                   nuclease
                                                                                                                                     detection
                                                                                                                                                                                                                                                                                                                                                                                                Shigella;
                                    cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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oligonucleotide

containing

sequence

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RESULT 4
AAA49863/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
     rpoB (rifampin resistance) gene (bp2161-2640). Amplification an cycle sequencing primers (see AAA49823-62) are used for the dete and analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC
                                                                               Disclosure;
                                                                                                   Method for the detection and tuberculosis with antibiotic
                                                                                                                                                                                                       11-DEC-1998;
                                                                                                                                                                                                                            10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis rpoB gene (rifampin resistance).
                                                                                                                                                                                 (VISI-) VISIBLE
                                                                                                                                                                                                                                                  22-JUN-2000
                                                                                                                                                                                                                                                                        WO200036142-A1
                                                                                                                                                                                                                                                                                                                    primer_bind
                                                                                                                                                                                                                                                                                                                                                     primer_bind
                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                           Antibiotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCR amplification was used to obtain rpoB genes from rifampicin-resistant Mycobacterium leprae strains. A comparison with the sequence of the rpoB gene from sensitive strains (AAQ51532) revealed mutations in the region encoding amino acids 400-450. The corresp. region was isolated from M.tuberculosis (AAQ61457). A common mutation seen in resistant strains occurs at codon 425 where Ser is
                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA49863;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAA49863 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCR amplification was used to obtain rpoB resistant Mycobacterium leprae strains. A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             þу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       isoniazid, rifampicin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 tacggcgtttcgatgaaccc
                                                   present sequence is that of the Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detecting mutation in
                                                                                                                                    2000-431611/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACGGCGTTTCGATGAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   detection of antibiotic resistance in Mycobacteria - azid, rifampicin or streptomycin resistance in tubercu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                          resistance;
                                                                             Page
mabA (isoniazid),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B₽;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                    tuberculosis
                                                                                                                                                                                                      980S-0111794
                                                                                                                                                                                                                           99WO-CA01177
                                                                                                                                                                                 GENETICS INC
                                                                                                                                                                                                                                                                                                                   /note= "372..391
                                                                            5; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                 complement(41..60)
                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                         /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               frequently by Leu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA; 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; 139 C; 148 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                           "primer of AAA49823"
                                                                                                                                                                                                                                                                                                                                                                                                         rpoB
                                                                                                                                                                                                                                                                                            "primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          katG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP.
                                                                                                                                                                                                                                                                                                                                                                                                         gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                  characterization of Mycobacterium resistance in a sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score
Pred.
                                                                                                                                                                                                                                                                                             of.
rpsL/s12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpoB or rpsL genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                            AAA49824"
                                                                                                                                                                                                                                                                                                                                                                                                     rifampin resistance; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67
(streptomycin),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Τ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .0076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       432;
                               detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
         PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT
AAT29126/
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Best Local S
Matches 20
                                                                                                                                                                                                         30-AUG-1995;
09-NOV-1994;
09-MAR-1995;
07-JUN-1995;
                                                                                                         esp.
                                                                                                                   Cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis. These primers can be used in a method for the detection and characterization of M. tuberculosis present in a sputum sample. The method involves performing a sequencing procedure, with or without prior amplification, to detect the presence of M. tuberculosis, and if present to evaluate the rpob, katG, rpsL/sl2 and 23S genes for the presence of antibiotic-inducing mutations. If M. tuberculosis is detected, a second sequencing procedure is performed on the sample to evaluate additional genes for the presence of antibiotic resistance-inducing mutations. Genotypic
                                                                            Example
                                                                                                                                       WPI;
                                                                                                                                                         Oldenburg
                                                                                                                                                                    Brow
                                                                                                                                                                                                                                                           09-NOV-1995;
                                                                                                                                                                                                                                                                                                                    Mycobacterium
                                                                                                                                                                                                                                                                                                                                       Staphylococcus; identification;
                                                                                                                                                                                                                                                                                                                                                                                rpoB
                                                                                                                                                                                       (THIR-) THIRD
                                                                                                                                                                                                                                                                               23-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                    02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT29126 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                        AAT29126;
                                                                                                                                                                                                                                                                                                                                                   Escherichia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 480 BP; 89 A; 153 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    antibiotic treatment options
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tests are rapid, sensitive and accurate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           451
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م
                                                                                                                                                                   MAD,
                                                                                                                                      1996-259862/26
                                                                                                                                                                                                                                                                                                                                                           mutant;
                                                                                                         'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tacggcgtttcgatgaaccc
                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACGGCGTTTCGATGAACCC
                                                                            33;
                                                                                                          human
                                                                                                                   of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                         Dahlberg
MC, Olive
                                                                                                                                                                                                                                                                                                                                                                             fragment (mutant) from
                                                                                                        nucleic
an p53 ge
                                                                          Page 306; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                  mutation; cleav
Saccharomyces;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                     WAVE TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                         95US-0520946.
94US-0337164.
95US-0402601.
95US-0484956.
                                                                                                                                                                                                                                                                                                                    tuberculosis
                                                                                                                                                                                                                                                          95WO-US14673
                                                                                                        gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA; 620
                                                                                                                  acids
                                                                                                                                                         JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                     cleavage; nuclease;
yces; Campylobacter;
fication; detection;
                                                                                                         ç
                                                                                                      to detect root identify
                                                                                                                                                                  Fors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                 ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20;
Pred. No.
                                                                                                                                                                                      INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium
                                                                                                                                                                  Heisler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ر.
ق
                                                                                                      mutation(s)
strains of r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0.0075
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŧ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           providing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB
                                                                                                                                                                 ĽM,
                                                                                                                                                                                                                                                                                                                                       ds
                                                                                                                                                                                                                                                                                                                                               Mycobacterium; Shigella;
                                                                                                                                                                                                                                                                                                                                                         cleavase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                other;
                                                                                                    microorganisms
                                                                                                                                                                Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                             tuberculosis
                                                                                                                allows detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             information
                                                                                                                                                                                                                                                                                                                                                        Thermus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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Selected from the group consisting of Cleavase (NLF) Selected from the group consisting of Cleavase (NLF) Selected from the group consisting of Cleavase (NLF) Selected from the group consisting and the Saccharomyces cerevis polymerase, Escherichia coli ExoIII and the Saccharomyces cerevis Radi/Radil complex. The nucleic acid substrate is preferably an oligonucleotide containing a human p53 gene sequence or oligonucleotide containing a human p53 gene sequence are

cerevisiae

Cleavage

of nucleic acids

ds using an enzyme, especially consisting of Cleavase (RTM)

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RESULT
AAA49826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 165/rrs
(clarofloxacin) ambA (ethambutol), pncA (pyrazinamide), gyrA
(ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
Chese primers can be used in a method for the detection and
characterization of M. tuberculosis present in a sputum sample.
Characterization of M. tuberculosis present in a sputum sample.
Characterization of M. tuberculosis present in a sputum sample.
Characterization of M. tuberculosis present in a sputum sample.
Characterization of M. tuberculosis present in a sputum sample.
Characterization of M. tuberculosis and if present to evaluate the presence of M.
Characterization, to detect the presence of M.
Characterization, to detect the presence of M.
Characterizations and if present to evaluate the rpoB, katG, rpsL/s12
and 23S genes for the presence of antibiotic-inducing mutations.
Clarify the control of the sample to evaluate additional genes for the presence of antibiotic resistance-inducing mutations. Genotypic tests are rapid, sensitive and accurate providing information as to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is that of the Mycobacterium tuberculosis rpoB (rifampin resistance) gene amplification primer rpoB-R (bp 2611-2592). It is used with the forward primer given in AAA49823 and with the sequencing primers given in AAA49825 and AAA49826 for the detection and analysis of antibiotic resistance-associated mutations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  analysis of antibiotic resistance-associated mutations in regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of the rpoB gene (see AAA49863). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and
The present sequence is that of the Mycobacterium tuberculosis
                                                            Claim 4; Page 5; 43pp; English.
                                                                                                                               Method for the detection and characterization of Mycobacterium tuberculosis with antibiotic resistance in a sample - \,
                                                                                                                                                                                                                                         WPI; 2000-431611/37.
                                                                                                                                                                                                                                                                                                                                                                        (VISI-) VISIBLE GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200036142-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Antibiotic resistance; rpoB gene; rifampin resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA49826 standard; DNA; 20 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 4 A; 6 C; 5 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibiotic treatment options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 tacggcgtttcgatgaaccc 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 4; 43pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tuberculosis rpoB gene sequencing primer rpoB-3s
                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0111794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-CA01177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.0095
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RESULT 3
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR (isoniazid), rpsL/s12 (streptomycin), 165/rrs (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis. These primers can be used in a method for the detection and characterization of M. tuberculosis present in a sputum sample. The method involves performing a sequencing procedure, with or without prior amplification, to detect the presence of M. tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12 and 23S genes for the presence of antibiotic inducing mutations. If M. tuberculosis is detected, a second sequencing procedure is performed to the sample of the presence of antibiotic inducing mutations.
                                                                                                                                                                                               17-SEP-1992;
30-APR-1992;
14-AUG-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rpoB (rifampin resistance) gene sequencing primer rpoB-3s (bp 2611-2592). It is used with the forward primer given in AAA49825 and with the amplification primers given in AAA49823 and AAA49824 for the detection and analysis of antibiotic resistance-associated mutations of the rpoB gene (see AAA49863). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and
                                                                                                          (INSP )
(MEDI-)
(UYBE-)
                                                                                                                                                                                                                                                        30-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                        rifampicin;
mutant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                M.tuberculosis rpoB gene fragment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ61457 standard; DNA; 432 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 20 BP; 4 A; 6 C; 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibiotic treatment options.
                                                                                                                                                     (ASSI-)
                                                                                                                                                                                                                                                                                    11-NOV-1993
                                                                                                                                                                                                                                                                                                               W09322454-A
                                                                                                                                                                                                                                                                                                                                          Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                              17-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              performed on the sample to evaluate additional genes for the presence of antibiotic resistance-inducing mutations. Genoty
                                                                                                                                                                                  16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tests are rapid, sensitive and accurate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 tacggcgtttcgatgaaccc
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20; Conserv
                                                                                                                         MEDICAL RES
                                                                                                                                                     ASSISTANCE PUBLIQUE.
                                                                                                                                         INST PASTEUR.
                                                  Cole
Zhang
                                                                                                                                                                                                                                                                                                                                                                                    antibiotic; susceptibility; sensitive; resistant; rpoB;
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                                                                                               CURIE PARIS VI P & M.
                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                             BERNE
                                                                                                                                                                                92FR-0011098.
92US-0875940.
92US-0929206.
93FR-0004545.
                                                                                                                                                                                                                                                        93WO-EP01063
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                                                                   Heym
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                                                                   Honore N,
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Pred. No. 0.0095;
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Perfect score:
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                                                                                                                                                                                        Ö
                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                        Score
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length: 2000000000
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Gapop 60.0 , Gapext 60.0
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Copyright (c) 1993 - 2000 Com
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                      AAA49863
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ABL/26802	AAS94186	AAZ38124	AAS92789	AAS92952	AAF89013	AAC32775	AAC48699	AAH53127	AAH68314	AAV74720	84	AAS87269	AAF27618	AAF71326	AAC90901	AAV04619	AAS94185	AAC90900	AAV04618	AAF61568	AAT13651	AAF61643	ABL18446	ABL33903	AAX13246	ABL18447	ABL32551	AAS52892	AAS51357	AAQ51532	~	AAT12096	999	46	AAH02079
Drosophila melanog	DNA encoding novel	Human FATP variant	DNA encoding novel	coding	سو		rabidopsis th	-	qlutamicum c	$^{\circ}$	lano	d nove	Mevalonate pathway	nebacterium q	aminopeptida	aminopeptida	encoding nove	aminopeptida	tida	lus cas	res	Lactobacillus case	hila me		Enterococcus faeca			faec	terococcus f	leprae rpoB	vcobacterium tub	tuberculosis r	is r	tub	Mycobacterium tube

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ALIGNMENTS

RESULT AAA49824 11-DEC-1998; 22-JUN-2000. Antibiotic Mycobacterium tuberculosis rpoB gene amplification primer rpoB-R. (VISI-) VISIBLE GENETICS INC 10-DEC-1999; WO200036142-A1 Mycobacterium tuberculosis. 25-SEP-2000 (first entry) AAA49824; AAA49824 standard; DNA; 20 BP Н resistance; rpoB gene; rifampin resistance; PCR primer; 98US-0111794. 99WO-CA01177

Method for the detection and characterization of Mycobacterium tuberculosis with antibiotic resistance in a sample $\boldsymbol{\cdot}$

WPI; 2000-431611/37.

gene

CDS

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ARSAGQDPRLDGHVERLRPQLGDLDTIGYRARKIAEDICLALQGSLLVRHGHPAVAEA
FLATBLGGORGGAYGTMPAGLDLAPILERALVKG"

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/gene="MT0701"
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PID:457174 PID:537028; identified by sequence similarity;
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ANGGGCGRPAREOYDDIGFYBAVYADIANNYSIDPARYYYTGSNGALMSYTLACNT
SIFAAIGYYSGTQLDPCSPRPSYLHIHGTADPLVRYHGGPGAGFARIDGPPYDDLO
AFWREVNRCGALDTTTEGPYTTSGATCADNRRVYLLTYDDAGHRWPSFATQTLWRFFA
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14439. .15161
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                                                                                                                                                                                                                                                                                                                                                                                  14439.
/product="hypothetical protein"
                                                                                                                                                            note="identified"
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gene

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gene

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                                  Matches
                                          Query Match
Best Local :
1709 TACGGCGTTTCGATGAACCC
         1 tacggcgtttcgatgaaccc
                                   20;
                                          Similarity
                                   Conservative
                                          100.0%;
1690
                 20
                                   0;
                                          Score 20; DB 1 
Pred. No. 0.06;
                                   Mismatches
                                                  DB 1;
                                   0;
                                                   Length 19352;
                                   Indels
                                   0;
                                   Gaps
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Search completed: August 7, 2002, 23:49:04 Job time: 9218 sec

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JOURNAL
REFERENCE
AUTHORS
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AUTHORS
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Whole genome comparison of Mycobacterium tuberculosis clinical and
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Mycobacterium tuberculosis CDC1551.

Mycobacterium tuberculosis CDC1551.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 19352)
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2 /hases 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (25-APR-2001) The Institute for Genomic Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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a 1534 c 1691 g 890 t
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gene

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putative"

gene

gene

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is not the result of a sequencing artifact; identifical interest putative; conserved hypothetical protein, authentic frameshift"

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CDS

/note="identified PF01261"

γď match ť PFAM

protein family HMM

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.10925

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GLECERI FEGPTENDECYCKY KRVEFKGI I CERGGVEVTRAKVRERMGHIELAPVT
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gene

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JOURNAL
REFERENCE
AUTHORS
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AUTHORS
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Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Corynebacterineae; Mycobacteriaceae;
Actinomycetales; Corynebacterium tuberculosis complex.
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U12205
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Mycobacterium tuberculosis H37Rv RNA-polymerase beta
gene, partial cds.
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Cole,S., Schopfer,K. and Burkart,T.
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Similarity 100.0%;
20; Conservative (
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Mycobacterium tuberculosis RNA polymerase beta'-subunit (r
gene, complete cds and RNA polymerase beta'-subunit rpoC
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Miller, L.P., Crawford, J.T. and Shinnick, T.M.
The rpoB gene of Mycobacterium tuberculosis
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L27989
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TEKGTFIINGTERVVVSQLVRSPGVYEDETIDKSTDKTLKSVKY IPSRGAMLEEDVDK
RDTVQVRIDBKRRQPVTVLLKALGWTSEG IVEREGFSBIMRSTLEKDNTVGTDEALLD
IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
EEDDVATIEYLDVELTPQTLNIFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
EEDDVATIEYLDVEATPQTLNIFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
MSRHERVVAERMTTODVEATFPQTLNIFFVVAAIKEFFGTSQLSQFDQNNPLSGLT
HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRNCPIETPEGPNLGLIGSLSVYARVNP
FGFIETPYRKVVDGVVSDEIVYLTADEEDRHVVAQANSPIDANGRFVEBRVLVRRKAG
EVEYVPSSEVDYNDVSPRQMVSVATAMIPFLEHDDANGRAVBRAKAGRSHNGTC
ANQCPIVDAGDRVEATSSQESGVIEEVSADVLTVMHNNGTRRTYRMKKARARSHNGTC
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ANQCPIVDAGDRVEATSSQESGVIEEVSADVLTVMHNNGTRRTYRMKKARARSHNGTC
ANQCPIVDAGDRVEATAMIPGGEMLLARIFGEKAREVADTSLKVPHGESGKVIGIRVESRED
DILVGKVTPKGETELTPEERLLRAIFGEKAREVADTSLKVPHGESGKVIGIRVESRED
EDELPAGVNBLVRVYVAQKKKISGGOKLAGRHGNKGVIGKILPVEDDFLADGTPVDI
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1065. .4598
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/prottein_id="AAA21417.1"
/db_xref="GI:537608"
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                                                                                                                                                                                                                                                           TIKSDDTVGRVKVYEAIVKGENIPEPGIPESFKVLLKELQSLCLNVEVLSSDGAAIEL
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/evidence=experimental
/product="RNA polymerase beta-subunit"
/protein_id="AAA21416.1"
/db_xref="GI:468334"
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                                                                                                       /codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MLEGCILADSRQSKTAASPSPSRPQSSSNNSVPGAPNRVSFAKL/
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/strain="Rv"
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Pred. No. 0.057;
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Submitted (20-APR-1998) Division of Infectious Disease, Affymetrix,
3180 Central Expressway, Santa Clara, CA 95051, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gingeras, T.R., Ghandour, G., Wang, E., Berno, A., Small, P.M., Drobniewski, F., Alland, D., Desmond, E., Holodniy, M. and Drenkow, J. Simultaneous genotyping and species identification using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex. 1 (bases 1 to 705)
                                                                                                                                                                                                 AR149128
Sequence
AR149128
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Gingeras,T.R., Ghandour,G., Wang,E., Be
Drobniewski,F., Alland,D., Desmond,E.,
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               of microorganisms Patent: US 6228575-A 24 08-MAY-2001;
                                               Gingeras,T.R., Mack,D., Chee,M.S., Berno,A.J., St
Ghandour,G. and Wang,C.
Chip-based species identification and phenotypic
                                                                                                 Unclassified.
1 (bases 1 to 706)
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                                                                                                                                                                                                                                                                                                                                                                              th 100.0%; Similarity 100.0%; 20; Conservative (
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/transl_table=11
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EVEYVPSSEVDYMDVSPRQMYSVATAMIFFLEHDDANRALMGANMQRQAVPLVRSEAP
LVGTGRELRAAIDAGT"
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/db_xref="taxon:1773"
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Location/Qualifiers
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                                                                                  Berno, A.J., Stryer, L.,
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Drenkow,J.
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                                                                                                                                                                                                                                                                                                                                              20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Detection of a genetic locus encoding resistance mycobacterial cultures and in clinical specimens Patent: US 5643723-A 1 01-UUL-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1 from patent US 150706
                                                                                                                                                                                   Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Bacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
                                                                                                                                                                                                                                              Sequence 2072 from Pate:
AX111339
AX111339.1 GI:13927631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 970)
Persing, D.H., Hunt, J.J.,
and Whelan, A.Christian.
                                                                                                                                   Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Picard, F.J. and Roy, P.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unknown.
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                                                                                 for detection of microorganisms Patent: WO 0123604-A 2072 05-APR-2001; Infectio Diagnostic (I.D.I.) INC. (CA)
                                                                                                                      Highly conserved genes and their use to
                                                                                                                                                                                                                                                                                     AX111339
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                                                                                                                                                                       Mycobacterium; Mycobacterium
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227 c 250 g
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                                 /organism="Mycobacterium
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302 c 330 g
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Pred. No. 0.055;
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ht WO0123604.
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Sequence 138
AR062059
AR062059.1
                                                                                                  1 (bases 1 to 620)

Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.

Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.

Cleavage of nucleic acid acid using thermostable methoanococcus

Jannaschii FEN-1 endonucleases

Patent: US 5843669-A 138 01-DEC-1998;
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20; Conserv
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Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N. Cleavage of nucleic acid acid using thermost jannaschii FEN-1 endonucleases

Patent: US 5843669-A 137 01-DEC-1998;
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Patent: US 5843669-A 136 01-DEC-1998;
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RESULT 9
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AR062061
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AR062060
   Mycobacterium
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Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.
Cleavage of nucleic acid acid using thermostable
Jannaschii FEN-1 endonucleases
Patent: US 5843669-A 140 01-DEC-1998;
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20; Conserv
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Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.

Cleavage of nucleic acid acid using thermostable methoanococcus

jannaschii FEN-1 endonucleases

Patent: US 5843669-A 139 01-DEC-1998;
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/replace="t"
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INIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDV
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/replace="a"
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l Similarity 100.0%;
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Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.
Cleavage of nucleic acid acid using thermostable methoanococcus
jannaschii FEN-1 endonucleases
Patent: US 5843669-A 135 01-DEC-1998;
Unclassified.

1 (bases 1 to 620)

Kaiser,M.W., Lyamichev,V.I. and Lyamichev,N.

Cleavage of nucleic acid acid using thermostable methoanococcus
                                                                                          Sequence 136
AR062057
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1 (bases 1 to 432
Heym, B., Cole, S.,
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AF146518
SCU06465
AF067447
AF214568
AF146044
AF14604181
CEF114A5
AX34545
AX34545
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AX346805
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AC048639
AB044172
FHEFHMDA
ATHTUBA6A
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AR067448
AR062056
AR062057
AR062058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AR062061
AF062033
AR149128
AF061333
AR111339
AF0112205
AF06266
AF172323
AF0608100
                                                                                                                                                                                                                                               ALIGNMENTS
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AE008100 Agrobacte
AE009134 Agrobacte
AL596159 Listeria
AF277396 Crithidia
247191 Calothrix D
AF080428 Agrocybe
AF080421 Agrocybe
AF325874 Staphyloc
M63306 S.flexneri
AC048639 Giardia 1
AE044172 Yamagishi
L36247 Fasciola he
M84699 Arabidopsis
L36248 Fasciola he
X68400 R.norvegicu
AF146518 Rattus no
U06465 Saccharomyc

U06465 Saccharomyc
AR067447 Sequence
AF214568 Rattus no
AF146044 Rattus no
AY069181 Drosophil
Z75951 Caenorhabdi
AX345453 Sequence
AX348335 Sequence
AX34835 Sequence
AX34605 Sequence
AX34605 Sequence

/organism="Mycobacterium tuberculosis" /strain="H37"	an Thos
	EATURES
tuberculosis Antimicrob. Agents Chemother. 341, 647-650 (1993)	JOURNAL
Colston, J., Matter, L., Schopfer, K. and Bodmer, T. Detection of rifampicin-resistance mutation in Mycobacterium	TITLE
Telenti, A., Imboden, P., Marchesi, F., Lowrie, D., Cole, S.T.,	AUTHORS
Mycobacterium; Mycobacterium tuberculosis complex. 1 (bases 1 to 432)	REFERENCE
Actinomycetales; Corynebacterineae; Mycobacteriaceae;	
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;	
	ORGANISM
Mycobacterium tuberculosis (strain H37) DNA.	SOURCE
RNA polymerase beta-subunit; rifampicin resistance.	KEYWORDS
L05910.1 GI:149991	ERSION
resistance gene, complete cds.	CCESSION
Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin	DEFINITION
MSGRIFRNAP 432 bp DNA linear BCT 21-MAY-1993	cocus
3/c	4SGRIFRNAP/c
	RESULT 1

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JOURNAL
MEDLINE
COMMENT
Search completed: August 7, 2002, 23:12:33 Job time: 11072 sec
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Best Local Similarity 100
Matches 15; Conservative
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20568492
On Aug 17, 1999 this sequence version replaced gi:5735350.
On Aug 17, 1999 this sequence version replaced gi:5735350.
Contact: Brian Oliver
Laboratory of Cellular and Developmental Biology
NIDDK, National Institutes of Health
6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 20892 USA
Fax: (301) 496 5239
Email: Oliver@helix.nih.gov,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www.niddk.nih.gov/intram/people/boliver.htm
Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
and analyses performed by National Institutes of Health Intramural
sequencing Center (NISC; see http://www.nisc.nih.gov).
Plate: 07 row: c column: 12
Seq primer: MI3RPl reverse primer (ABI).
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                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="1-5 day adult"
//dev_stage="1-5 day adult"
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//site_1: ECOR I; Site_2: Xho I; Testes dissected from 1-5
//day adult y[*] w[67c1]/Y males raised at 25oC. RNA
//solated using Trizol (Life Technologies) and a single
//round of Poly(A)+ selection using Oligotex (Olagen). CDNA
//sit: Oligo dT-primed, Size fractionated -1-6 kb, and
//directionally cloned at EcoRI and XhoI in Uni-ZAP XR.
//Following a single round of amplification pBlueScript SK
//phagemids were mass excised. A distribution channel for
//clones is being sought, but not currently available.
//Requests for clones cannot be honored."
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/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Drosophila melanogaster"
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                                                                                                                                                                                                                                                                                    75.0%;
                                                                                                                                                                                                                                                                                    Score 15; DB 9; L; Pred. No. 2.4e+02;
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                                                                                                                                                                                                                                                                                                            Length 379;
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REFERENCE
AUTHORS
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VERSION
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AI945868
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BE423869/c
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                              6 tcggcgagctgatcc
                                                                                                                                                                                                                                                                                                                                                          TCGGCGAGCTGATCC
                     Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscommorbha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                  A1945868 376 bp mRNA linear EST 08-JAN-200: bs17g07.yl Drosophila melanogaster adult testis library Drosophila melanogaster cDNA clone bs17g07 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The structure and function of the expressed portion of the wheat genomes - Endosperm cDNA library Unpublished (2000)
Contact: Olin Anderson Us Department of Agriculture, Agriculture Research Service, Pacif West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773
  Andrews, J.,
                                                                                                                                                 EST
                                                                                                                                                                    AI945868
AI945868.2
                                                                                                                                                                                                                                                                                                                                                                                                                                            15; Conserv
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Seq primer: Stratagene SK primer.
Location/Qualifiers
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Altenbach, S., Anderson, O.D., Chao, S., Galili, G., Han, P.S., Hsia
, C.C., Kang, Y., Lazo, G.R., Miller, R., Rausch, C.J., Seaton, C.L. and
Tong, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BE423869 237 bp mRNA linear EST 24-JUL-2: WHE0067_F05_K09ZS Wheat endosperm cDNA library Triticum aestivum cDNA clone WHE0067_F05_K09, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence have been trimmed to remove vector quality sequence with phred score less than
                                                                                                                             fruit fly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: oandersn@pw.usda.gov
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79 c 40 g 53 t
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/lab_host="E. coli SOLR"
/lab_host="E. coli SOLR"
/note="Vector: Lambda ZAP II, excised phagemid: Site_1:
ECORI: Seeds collected, endosperm isolated, and RNA
ECORI: Seeds collected, rehouse contented by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Wheat endosperm cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Cheyenne"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Triticum aestivum"
                                                                                                                                                                      GI:9991196
Bouffard, G.G.,
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100.0%;
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Pred. No.
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Cheadle, C.,
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. 2.3e+02;
Lu,J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 237;
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Becker, K.G.
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  Gene discovery using transcription in the
                                                                                                                                                                                                                                                                                         A1944952 379 bp mRNA bs07c12.yl Drosophila melanogaster adult melanogaster cDNA clone bs07c12.5', mRNA A1944952
                                                                                                                 Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                   Oliver, B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Aug 17, 1999 this sequence version replaced gi:5736266 Contact: Brian Oliver Laboratory of Cellular and Developmental Biology NIDDK, National Institutes of Health 6 Center Drive MSC 2715, Bldg 6, Rm B1-13, Bethesda, MD 26 Fax: (301) 496 5239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oliver, B. Gene discovery using computational and microarray analysis of transcription in the drosophila melanogaster testis Genome Res. 10 (12), 2030-2043 (2000)
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Seq primer: M13RP1 reverse primer (ABI).
Location/Qualifiers
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Tissue isolation and library construction performed at the National
Institute of Diabetes and Digestive and Kidney Diseases, NIH (see
http://www.niddk.nih.gov/intram/people/boliver.htm). DNA sequencing
                                                                     Andrews, J., Bouffard, G.G., Cheadle, C.,
                                                                                                                                                                                                                      fruit fly.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                             (bases 1 to 379)
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Site_1: ECCR I; Site_2: Xho I; Testes dissected from 1-5
day adult y(*) w(67c1)/Y males raised at 250C. RNA
isolated using Trizol (Life Technologies) and a single
round of Poly(A)+ selection using Oligotex (Olagen). cDNA
library constructed using Stratagene ZAP-cDNA syntesis
kit. Oligo dT-primed, size fractionated -1-6 kb, and
directionally cloned at EccRI and XhoI in Uni-ZAP XR.
Following a single round of amplification pBlueScript SK
phagemids were mass excised. A distribution channel for
clones is being sought, but not currently available.
Requests for clones cannot be honored."

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/strain="y[*] w[67cl]/Y"
/db_xref="taxon:7227"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Drosophila melanogaster adult testis library"
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100.0%;
computational and microarray analysis drosophila melanogaster testis
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Pred. No.
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hes 0;
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testis library
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                                                                       Becker, K.G.
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sected from 1-5
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Clark,M., Aanstad,P., Hennig,S., Johnson,S.L. and Lehrach,H.

EST sequencing of a zebrafish shield stage cDNA library normalised by oligonucleotide fingerprinting Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Hennig S
Laboraty 123, dept.Lehrach
Max-Planck-Institut fuer Molekulare Genetik
Thnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1612
Fax: +49 30 8413 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Danio rerio
Eukaryota; Metazoa; Chordata; Craniata;
Actinopterygii; Neopterygii; Teleostei;
; Cyprinidae; Danio.
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MPMGP637 Danio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: hennig@molgen.mpg.de 5' EST sequencing of clones
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/note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI;
/note="Vector: pZIPLOX; Site_1: NotI; Site_1: NotI; Site_2: SalI;
/note="Vector: pZIPLOX; Site_1: NotI; 
                            /Clone="MPMCp637,18E17;MPMGp637E1718"
/Clone_lib="Zebrafish shield stage whole embryo cDNA
/library MPMCp637"
/tissue_type="whole embryo"
/dev_stage="shield stage, 6 hrs post-fertilisation"
/lab_host="E.coli, XLI blue MRF"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI;
oligo-dT-NotI primed, SalI adaptors, directionally cloned,
library normalised by oligonuclectide fingerprinting"
a 152 c 139 g 139 t 1 others
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/sex="mixed male and female"
/tissue_type="brain"
/dev_stage="adult"
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/db_xref="taxon:7955"
/clone="5333151"
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/db_xref="taxon:7955"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: John Fellers
Contact: John Fellers
US Department of Agriculture, Agriculture Research Service, Plant
Science and Entomology Unit
Science and Entomology Unit
Dept. of Plant Pathology, 4006 Throckmorton Hall, Kansas State
University, Manhattan, KS 66506, USA
Tel: 785-532-2367
Fax: 785-532-6167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pellers,J.P., Li,W.L., Hill-Ambroz,K., Matthews,A. and Gill,B.S. The structure and function of the expressed portion of the wheat genomes - Kansas State University. Fusarium graminearum infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Magnoliophyta; Eliliopsida; Triticeae; Triticum.

1 (bases 1 to 700)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: jpf@alfalfa.ksu.edu
Sequence have been trimmed
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                                                                                                                            Plants were grown in the greenhouse. Spikes were sprayed with Fusarium graminearum (at what stage). Total RNA, and poly(A) RNA were prepared from infected spikes. cDNA was prepared using the SmartTM PCR cDNA synthesis kit from Clonetech. cDNA was cloned into the pGEM-T easy vector from Promega."
                                                                                                        from Promega.
                                                                                                                                                                                                                                                                                                           cDNA library"
                                                                                                                                                                                                                                /tissue_type="Spike"
/dev_stage="Adult plant"
/lab_host="E. coli JM109"
/note="Vector: pGEM-T easy;
                                                                                                                                                                                                                                                                                                                          /clone_lib="KSU wheat Fusarium graminearum infected
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                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:4565"
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/cultivar="Sumai3"
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a; Poales; Poaceae; Pooideae
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Tetrahymena thermophila.
Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymen
Hymenostomatida; Tetrahymenina; Tetrahymena.
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                                                                                                                                                                                      Tetrahymena thermophila
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920 E. 58th Street, Chicago,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2002)
Contact: Turkewitz AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 132)
Turkewitz, A.P., Kar
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                                                                                                                                      BM398255.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hymenostomatida;
1 (bases 1 to 1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: apturkew@midway.uchicago.edu
Seq primer: T3.
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/db_xref="taxon:5911"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
/note="Vector: BlueScript2 SK+; Details on
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/strain="CU428.1"
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                             Oligohymenophorea;
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Turkewitz,A.P., Karr,
J. and Klobutcher,L.
EST from Tetrahymena
Unpublished (2002)
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fu53f08.yl:
similar to
                                                    Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Email: zbrafish@watson.wustl.edu
EDNA Library Preparation: John Ngai. cDNA Library Arrayed by:
Matthew Clark. DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
Missouri (web address: www.genomesystems.com) (email contact:
Info@genomesystems.com) and Research Genetics, Huntsville, Alabama
(web address: www.resgen.com) (email contact: info@resgen.com) and
                                                                                                                                                                                                                                                                                                                                                                                     Clark,M., Johnson,S.L., Lehrach,H., Lee,R., Li,F., Marra,M., J., S., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylle,T., Undar, K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Watersty
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University of Chicago
920 E. 58th Street, Chicago,
Tel: 773 702 4374
Fax: 773 702 3172
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Other_ESTs: fu53f08.xl
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                     www.rzpd
                                   RessourcenZentrumPrimarDatenbank, Berlin,
                                                                                                                                                                                                                                                                                  Contact: Stephen L. Johnson
                                                                                                                                                                                                                                                                                                                                             WashU Zebrafish EST Project 1998
                                                                                                                                                                                                                                                                                                                                                                      and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B1981973.1
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16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                   S., Shin, T., Jackson, Y.,
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/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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/strain="CU428.1"
/db_xref="taxon:5911"
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TR:Q9Y4D4
sequence stop: 446
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Ostariophysi; Cypriniformes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG299722 828 bp mRNA linear EST 17-OCT-2001
HVSMEa0021120f Hordeum vulgare seedling shoot EST library
HVGNNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0021120f,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             l Similarity
17; Conser
                                                                                                                                                                                                                                                                                                                                Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, US
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W., Fenton,R.D. and Main,D.
Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea; Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BG299722.1 GI:13087434
                                                                                                                                                                                                                                                                                Email: rwing@clemson.edu
Total hg bases = 574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for barley genomics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hordeum vulgare
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                                                                                                                                                                                                  primer: AATTAACCCTCACTAAAGGG
h quality sequence stop: 643.
Location/Qualifiers
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/dev_stage="five day old etiolated seedling"
/"-" host="E. coli DH10B"
/"-" bost="E. coli DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wing RA
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                        /clone_lib="Hordeum vulgare seedling shoot EST library
HVcDNA0001 (Cold stress)"
                                                                      /clone="HVSMEa0021120f"
                                                                                                   /db_xref="taxon:4513"
                                                                                                                              /cultivar="Morex"
/tissue_type="Seedling
                                                                                                                                                 organism="Hordeum vulgare"
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B; Pred. No. 22;
O; Mismatches
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shoot"
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RESULT BG299722

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ACCESSION VERSION

SOURCE

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REFERENCE

AUTHORS

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JOURNAL

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FEATURES

BASE COUNT ORIGIN

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BASE COUNT
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SOURCE
ORGANISM
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LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GETCGGCGAGCTGATCC 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 130)
Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E., Frankel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EST
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BM397871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM397871 130 bp mRNA linear EST 17 5009-0-38-C10.t.1 Chilcoat/Turkewitz cDNA (large fraction)
                                                                                                                                                                                                                                                                                                                        University of Chicago
920 E. 58th Street, Chicago, IL 60637, USA
                                                                                                                                                                                                                                                                                                                                                                                 Contact: Turkewitz AP
Molecular Genetics and Cell Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ,J. and Klobutcher,L.
EST from Tetrahymena
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetrahymena thermophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hymenostomatida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 172
                                                                                                                                                                                                              primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                               from Tetrahymena thermophila, strain CU428.1, growing cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /lab_host="TJC121"
/note="vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
/note="vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 50C for 2 days. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 600000 pfu were in vivo excised to give pBluescript SK(-) cDNA were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                             apturkew@midway.uchicago.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30.
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271 c
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/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
                                                                          /organism="Tetrahymena thermophila"
/strain="CU428.1"
/db_xref="taxon:5911"
                                                                                                                                                                                       Location/Qualifiers
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100.0%; Pr
0;
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1 c 220 g 165 t
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Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
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HVSMEh0088E21f Hordeum vulgare 5-45 DAP spike EST library
HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0088E21f,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: rwing@clemson.edu
Total hq bases = 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             On Jun 26, 2000 this sequence version replaced gi:13187931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
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Location/Qualifiers
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/lab_host="SOLR"
/lab_host="SOLR"
/lab_host="SOLR"
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
/note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1;
/note="Vector: Site_1: Site_1: Xho1;
/note="Vector: Site_1: Xho1;
/note: Site_1: Xho1;
/note: Site_1: Xho1;
/note: Site_1: Xho1;
/note: 
                                                                                                                                                                                                                                                                      /clone_lib="Hordeum vulgare 5-45 DAP spike HVcDNA0009 (5 to 45 DAP)" /tissue_type="5-45 DAP Spike"
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Hordeum vulgare"
/cultivar="Morex"
/db_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                              /clone="HVSMEh0088E21f"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                              Unpublished (2011) Anderson
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
Wash Area, Western Regional Research Conter
Wash Area, Western Regional Research Conter
Wash And Anchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l (bases 1 to 658)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library Unpublished (2000)
                                                                                                                                                                                         Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.
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                                                                                                                                                                                                                                                                                           oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" a 203 c 158 g 120 t 2 others
                                                        /cultivar="Chinese Spring"
/db_xref="taxon:4565"
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                          /clone="WHE1101_H10_O19"
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                                                                                                                                                                          Location/Qualifiers
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/clone_lib="Wheat etiolated seedling
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100.0%;
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22;
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root normalized cDNA
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1 (bases 1 to 544)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Olin Anderson
Content of Agriculture, Agriculture Research Service,
US Department of Agriculture, Center
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE445100 544 bp mRNA linear EST 25-WHE1132_H08_P16ZS Wheat etiolated seedling root normalized library Triticum aestivum cDNA clone WHE1132_H08_P16, mRNA
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17; Conserv
                                                                                                                                                                                                                                                                                                                      Sequence have been trimmed to remove vector quality sequence with phred score less than Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                           Email: oandersn@pw.usda.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                        /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1132_H08_P16"
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/lab_host="E. coli DH10B"
/dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                    /organism="Triticum aestivum"
                                                         'tissue_type="Root"
                                                                                                             'clone_lib="Wheat etiolated seedling root normalized
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BE444713
                                                                                                                                                                                                                                                                                                                                                                     Email: oandersn@pw.usda.gov
Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence
Sequence have been trimmed score less than 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (2000)
Contact: Olin Anderson
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han, P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

The structure and function of the expressed portion of the wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BE444713 558 bp mRNA linear EST 25-
WHE1137_H03_005ZS Wheat etiolated seedling root normalized
library Triticum aestivum cDNA clone WHE1137_H03_005, mRNA
                                                                                                                                                                                                                                                                                                                                         quality sequence with phred score less than Seq primer: Stratagene SK primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             genomes - Normalized root cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lab by D. Zhang at Texas Tech Univeristy. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      excised to give pBluescript phagemids before normalization was carried out. The mass excision phagemid library and normalization were done in HT
/dev_stage="Five day old etiolated seedling"
/lab_host="E.coli DHIOB"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
                                                                                                                                                                                    /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1137_H03_005"
                                                                                                                                  library"
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                                                                                                      /tissue_type="Root"
                                                                                                                                                           /clone_
                                                                                                                                                                                                                                                                    /organism="Triticum aestivum|
                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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BM396091 5009-0-17
BM398255 5009-0-42
B1991973 fu53f08.y
B1888442 EF637-2-0
BE585978 Est#777-0
BE423869 WHE0067_F
A1944952 bs07797.y
BH1894952 bs07797.y
BH194952 bs07797.5
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FEATURES SOURCE	AUTHORS TITLE JOURNAL COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE	RESULT 1 BE443802 LOCUS DEFINITION	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0
West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 510559573 Fax: 510559581B Email: condersn@pw usda gov Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer. Location/Qualifiers 1. 422 /organism="Triticum aestivum" /cultivar="Chinese Spring" /clone="WHE1122_B06_C12" /clone="WHE1122_B06_C12" /clone="Wheat etiolated seedling root normalized cDNA library" /tissue_type="Root"	nn,O.D., Chao,S., Choi,D.W., Close,T Hsia,C.C., Kang,Y., Lazo,G.R., Mill C.J., Seatcon,C.L., Tong,J.C. and Zh ucture and function of the expresse - Normalized root cDNA library shed (2000) :: Olin Anderson urtment of Agriculture, Agriculture	BE443802.1 GI:9443341 BE443802.1 GI:9443341 EST. bread wheat. Triticum aestivum Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum. 1 (bases 1 to 422)	7 2 3 0	15 75.0 652 10 BF489438 BF489438 AT2558.5 15 75.0 667 10 BF489430 BF489430 AT2558.5 15 75.0 667 10 BF489536 BF489536 AT2558.5 15 75.0 703 10 BF496035 BF489536 AT25583.5 15 75.0 703 10 BF496035 BF496035 AT09742.5 15 75.0 958 10 BE969326 BF969326 601649529 15 75.0 984 12 CNS01GJZ B4616363 HV5NEK001 15 75.0 1000 10 BG416363 B6416363 HV5NEK001 17 70.0 159 10 B1727507 C61884 C61884 C61884 Yuji 18 70.0 251 12 AQ906217 B1727507 1031093A0 14 70.0 251 12 AQ906217 AQ906217 GSSTC0226 14 70.0 299 10 B133481 BF920601 QVO NT015 14 70.0 299 10 B133481 B79472 B133481 U1-W-BH3 17 70.0 329 10 H57342 B133481 U1-W-BH3 18 70.0 329 10 H57342 B133481 U1-W-BH3 19 70.0 329 10 H57342 B133481 U1-W-BH3 10 70.0 329 10 H57342 B133481 U1-W-BH3 11 70.0 349 9 AJ281216 B24757 B133481 U1-W-BH3 11 70.0 349 10 B224757 B133481 B2347857 B3333 11 70.0 349 9 AJ281216 B24757 WHE2233_G 11 70.0 350 9 AV19317 AV193317 AV193317 AV193317 AV197881

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                  13-NOV-2000; 2000WO-US31152
                                                                                                                           Mycobacterium tuberculosis
                                                                                                                                                         Drug target; growth; organism viability; characterisation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying nucleotide or polypeptide sequence for use as drug target involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                                                                                                                                                      Sequence 3519 BP;
                                                                                                                                                                                                                                                                                                                                                     an organism.
                                                                                                                                                                                                                                                                                                                                                                                                                        algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleotical day and polypeptides that may characteristing the function of nucleotical day and polypeptides that may characteristic the court of t
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99US-0165124.
2000US-0179531.
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ilarity 100.0%;
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AAA49863
                                                                                                                                                          The present sequence is that of the Mycobacterium tuberculosis crops (rifampin resistance) gene (bp2161-2640). Amplification and cycle sequencing primers (see AAA49823-62) are used for the detection and analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 165/rrs (streptomycin), embB (ethambutch), pncA (pyrazinamide), yyrA (streptomycin), embB (ethambutch), pncA (pyrazinamide), yyrA (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis. These primers can be used in a method for the detection and characterization of M. tuberculosis present in a sputum sample. The method involves performing a sequencing procedure, with or without prior amplification, to detect the presence of M. tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12 and 23S genes for the presence of antibiotic-inducing mutations. If M. tuberculosis is detected, a second sequencing procedure is performed on the sample to evaluate additional genes for the presence of antibiotic resistance-inducing mutations. Genotypic tests are rapid, sensitive and accurate providing information as to
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                                    Query Match
Best Local S
Matches 20
                                                                                                                      Sequence 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA49863 standard;
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/note= "primer of AAA49823"
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    corresponding to each drug resistance detection probe, a contrast group probe corresponding to each drug resistance detection probe, and a marker for detecting a hybridisation of the oligonucleotide chip and a specimen. The identification probe is comprised of species-specific DNA sequences of mycobacterial rpoB gene and the detection probe is comprised of one or more modified codons of mycobacterial rpoB gene. The method involves amplifying rpoB gene fragments of specimen by Polymerase Chain Reaction (PCR) and discriminating species by fluorescent intensity corresponding to a particular species. The specimen is preferably uncultured sputum, blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569 represent mycobacterium generics identification.
                                                                                                                                                                                                                               The invention relates to a diagnostic kit for mycobacterial species identification and drug resistance detection comprising an oligonucleotide chip including a species identification probe, a mycobacterial drug-resistance detection probe, a contrast group promycobacterial drug-resistance detection probe, a contrast group pro
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                                                                                                                                                                                                                                                                                                                                                            Disclosure;
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represent mycobacterium
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; sputum; blood; cerebrospinal fluid; ;
                                                                                                                                                                                                                                                                                                                                                            English.
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Query Match Best Local S Matches 20

Similarity

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RESULT 1
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Best Local
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                                                                                                                                                                                                                                      30-APR-1992;
14-AUG-1992;
16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                       PCR amplification was used to obtain rpoB genes from rifampi resistant Mycobacterium leprae strains. A comparison with the resistant Mycobacterium leprae strains. A comparison with the requence of the rpoB gene from sensitive strains (AAQ51532) mutations in the region encoding amino acids 400-450. The corregion was isolated from M.tuberculosis (AAQ61457). A commor mutation seen in resistant strains occurs at codon 425 where
                                                                                                   bу
                                                                                                                                                                                                                                                                                30-APR-1993;
                                                                                                                                                                                                                                                                                                                                 Mycobacterium
                                                                                                                                                                                                                                                                                                                                                   mutant;
                                                                                                                                                                                                                                                                                                                                                                            M.tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                             AAQ61457;
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                                                                                                                    Rapid detection of antibiotic resistance in Mycobacteria
                                                                                                                                     P-PSDB;
                                                                                                                                             WPI;
                                                                                                                                                                     Bodmer T,
                                                                                                                                                                                              (MEDI-)
                                                                                                                                                                                                                                                                17-SEP-1992;
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Sequence
                substituted,
                                                                                                                                                                                      (UYPA-)
                                                                                                             soniazid, rifampicin
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DB; AAR51372.
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Zhang
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92US-0929206.
93FR-0004545.
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78
                                                                                   97pp; English.
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                                Kit for mycobacterial species identification and drug resistance detection, has oligonucleotide chip with species identification a mycobacterial drug-resistance detection probe, and its contrast
                                                                                                                                                                                                                                                                                                                     Drug resistance detection; mycobacterial species identification; oligonucleotide chip; rpoB; sputum; blood; cerebrospinal fluid; s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                corresponding to each drug resistance detection probe, and a marker for detecting a hybridisation of the oligonucleotide chip and a specimen. The identification probe is comprised of species-specific DNA sequences of mycobacterial rops gene and the detection probe is comprised of one or more modified codons of mycobacterial rops gene. The method involves amplifying rops gene fragments of specimen by Polymerase Chain Reaction (PCR) and discriminating species by fluorescent intensity corresponding to a particular species. The specimen is preferably uncultured sputum, blood or cerebrospinal fluid of a patient. Sequences AAS99478-AAS99569 represent mycobacterium species identification probes and primers of the
                                                                                            WPI; 2002-075472/10.
                                                                                                                                                                         30-MAY-2000;
                                                                                                                                                                                                  30-MAY-2001; 2001WO-KR00904
                                                                                                                                                (BIOM-) BIOMEDLAB CO
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                                                                                                                                                                                                                                                                                  Mycobacterium africanum
                                                                                                                                                                                                                                                                                                                                                            Mycobacterium species identification primer
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAS99527;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a diagnostic kit for mycobacterial species identification and drug resistance detection comprising an oligonucleotide chip including a species identification probe, a mycobacterial drug-resistance detection probe, a contrast group prol
                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS99527
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Disclosure;

Page

English

mycobacterial drug-resistance detection probe, a contrast group probe corresponding to each drug resistance detection probe, and a marker for detecting a hybridisation of the oligonucleotide chip and a specimen contentification probe is comprised of species-specific DNA sequences of

identification and drug resistance detection comprising oligonucleotide chip including a species identification

The invention relates to a diagnostic kit

for mycobacterial

species

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Disclosure;

Page 21;

74pp; English.

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Best Local
                                                                                                                              a mycobacterial drug-resistance
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                                                                                                                                                                                                                                                                                                                                                    Mycobacterium bovis
                                                                                                                                                                                                                                                                                                                                                                                      Drug resistance detect oligonucleotide chip;
                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium
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                                                                                                                                              detection,
                                                                                                                                                                                                                               (BIOM-)
                                                                                                                                                                                                                                                       30-MAY-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 306 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention.
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                                                                                                                           mycobacterial species identification and on, has oligonucleotide chip with species acterial drug-resistance detection probe,
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Best Local Similarity 100.0%;
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                This sequence represents a mycobacterial rpoB gene fragment, that is amplified using the PCR primers of the invention. The primers form a method of detecting and identifying mycobacterial species by constructing a phylogenetic tree for the species. The use of the primers for sequence-specific amplification of the rpoB gene (encoding the beta subunit of RNA polymerase) from mycobacterial species provides an efficient way of characterising these species. In addition to phylogenetic analysis, the rpoB gene can be used as an alternative to the 16S rRNA gene because it has four subunits, which are highly conserved throughout prokaryotes. The method is particularly useful for slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin susceptibility can be simultaneously determined in M. tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New pair of polymerase chain reaction (PCR) primers - for sequence-specific amplification of the rpoB gene from mycobacterial species, useful for detecting and identifying mycobacterial species
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RpoB gene; mycobacteria; phylogenetic tree construction;
mycobacterial species identification; phylogenetic analysis; ss
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              Mycobacteria bovis
                                         RpoB gene; mycobacteria; phylogenetic tree construction; mycobacterial species identification; phylogenetic analy
                                                                                 RpoB gene fragment.
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                                                                                                                                            AAX27180;
                                                                                                                                                                      AAX27180 standard; DNA; 306
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                                                                                                                                                                                                                                                                                                                                                                          56 A;
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                                                                                                                                                                                                                                                                                                                                                                          96 C;
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Pred. No. 0.025;
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Park M;

30-MAY-2000; 2000KR-0029369

(BIOM-) BIOMEDLAB CO LTD

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RESULT
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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 20; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence represents a mycobacterial rpoB gene fragment, that is amplified using the PCR primers of the invention. The primers form a method of detecting and identifying mycobacterial species by constructing a phylogenetic tree for the species. The use of the primers for a phylogenetic tree for the species. The use of the primers for sequence-specific amplification of the rpoB gene (encoding the beta sequence-specific amplification of the rpoB gene (encoding the beta sequence-specific amplification of the rpoB gene (encoding the beta sequence-specific amplification of the rpoB gene (encoding the beta sequence-specific amplification of the rpoB gene (encoding the beta sequence-specific amplification of the rpoB gene fragment, that is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New pair of polymerase chain reaction (PCR) primers - for sequence-specific amplification of the rpoB gene from mycobacterial species, useful for detecting and identifying mycobacterial species
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                                                                                                                                                                                                                                                              Drug resistance oligonucleotide
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                                                                                                             30-MAY-2001;
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                                                                                                                                                                               WO200192573-A1
                                                                                                                                                                                                              Mycobacterium tuberculosis.
                                                                                                                                                                                                                                               primer
                                                                                                                                                                                                                                                                                                                 Mycobacterium species identification primer #1.
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                                                                                                                                                                                                                                                             detection; mycobacterial species identification;
chip; rpoB; sputum; blood; cerebrospinal fluid; ;
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Pred. No. 0.025;
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RESULT
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Matches 20
This sequence represents a mycobacterial rpoB gene fragment, that is amplified using the PCR primers of the invention. The primers form a method of detecting and identifying mycobacterial species by constructing a phylogenetic tree for the species. The use of the primers for sequence-specific amplification of the rpoB gene (encoding the beta subunit of RNA polymerase) from mycobacterials species provides an efficient way of characterising these species. In addition to the 16s rRNA gene because it has four subunits, which are highly conserved throughout prokaryotes. The method is particularly useful for slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin susceptibility can be simultaneously determined in M. tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                               New pair of polymerase chain reaction (PCR) primers - for sequence-specific amplification of the rpoB gene from mycobacterial species, useful for detecting and identifying mycobacterial species
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                                                                                                                                                                                                                                                                                                                                                                             Claim
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Pred. No.
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0.031;
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Matches Query Match Best Local

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Similarity 100 20; Conservative

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                     phylogenetic analysis, the rpoB gene can be used as an alternative to the 16S rRNA gene because it has four subunits, which are highly conserved throughout prokaryotes. The method is particularly useful for slow growing, fastidious or uncultivatable mycobacteria. Also, rifampin susceptibility can be simultaneously determined in M. tuberculosis.
                                                                                     This sequence represents a mycobacterial rpoB gene fragment, that is amplified using the PCR primers of the invention. The primers form a method of detecting and identifying mycobacterial species by constructing a phylogenetic tree for the species. The use of the primers for sequence-specific amplification of the rpoB gene (encoding the beta subunit of RNA polymerase) from mycobacterial species provides an efficient way of characterising these species. In addition to
                                                                                                                                                                                                                            New pair of polymerase chain reaction (PCR) primers - for sequence-specific amplification of the rpoB gene from mycobacterial species, useful for detecting and identifying mycobacterial species
 Sequence
                                                                                                                                                                                                      Claim 4; Page 62-63; 91pp; English.
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                                                                                                                                                                                                                                                                                                                 Kim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacteria africanum.
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вP;
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56 A; 95 C; 108 G;
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Pred. No. 0.025;
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47 T; 0 other;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The antibiotic resistance spectrum (ARS) of a mycobacterium can be determined by amplifying the relevant part of the antibiotic resistance gene, i.e. the M. tuberculosis rpoB gene fragment amplified using the primer set AAT12091-98, hybridising it with a least 1 rpoB gene probe, detecting the hybrids formed and inferring the ARS, and opt. the spp., from the differential hybridisation patterns. The method is partic. useful for the detection of rifamplein and/or rifabutin resistance in M. leprae or M. tuberculosis, and mycobacterial spp. identification. The method is rapid and reliable and provides simultaneous determn.
        The present sequence is that of the Mycobacterium tuberculosis rpoB (rifampin resistance) gene amplification primer rpoB-F (bp 2201-2220). It is used with the reverse primer given in AAA49826 for the advection and analysis of antibiotic resistance-associated mutations of the rpoB gene (see AAA4983). Amplification and cycle sequencing primers (see AAA4982-62) have been developed for the detection and analysis of antibiotic resistance-associated mutations in defined analysis of antibiotic resistance-associated mutations in defined
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                                                                                                                              Claim 4; Page 4; 43pp;
                                                                                                                                                       tuberculosis
                                                                                                                                                                   Method for
                                                                                                                                                                                                                       Shipman
                                                                                                                                                                                                                                                                                                   10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                              tuberculosis
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                                                                                                                                                                                                                                                 GENETICS INC
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 katG (isoniazid),
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 oxyR-aphC
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                                           The present sequence is that of the Mycobacterium tuberculosis rpoB (rifampin resistance) gene sequencing primer rpoB-5s (bp 2201-2220). It is used with the reverse primer given in AAA49826 and with the amplification primers given in AAA49823 and AAA49824 for the detection and analysis of antibiotic resistance-associated mutations of the rpoB gene (see AAA49863). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), kat6 (isoniazid), cxyr-aphC PR
                                                                                                                                                                                                                                                                                                   WPI; 2000-431611/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200036142-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis rpoB gene sequencing primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA49825 standard; DNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibiotic treatment options.
                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                Method for the detection and characterization of Mycobacterium tuberculosis with antibiotic resistance in a sample -
                                                                                                                                                                                                                                                                                                                                                                                                    11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                     10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                 (VISI-) VISIBLE GENETICS INC
                             regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR (isoniazid), mabA (isoniazid), rpsL/sl2 (streptomycin), 16S/rrs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isoniazid), mabA (isoniazid),
               streptomycin), embB (ethambutol),
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Pred. No. 0.031;
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                 (pyrazinamide),
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(ciprofloxacin) and

(azithromycin)

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Result
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Gapop 60.0 , Gapext 60.0
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                               M. tuberculosis rp
Mycobacterium tube
Mycobacterium tube
RpoB gene fragment
RpoB gene fragment
RpoB gene fragment
RpoB gene fragment
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Mycobacterium tu	AA19968 AAV31045	19	205	70.0	14	45
Mycobacterium		3 N 3 N	4403765		7 J	44
Drosophila melanog	ABL1	23	4		15	42
Pseudomona		23	2772	•	15	41
Drosophila		23	2488	-	<u>, , ,</u>	40
B. subtilis	AAS02316	22	1092		15	9
Propionibacterium		23	27426		16	88
Mycobacterium		24	306		16	37
Mycobacterium	AAS9956	24	306	•	16	36
Mycobacterium	AAS9956	24	306		16) (L)
Mycobacterium	AAS99557	24	306		16	4.1
	AAS99539	24	306		16	i.u
	AAX27186	19	306			32
	AAX27183	19	306			i L
	AAX27182	19	306			30
	AAX27177	19	306			2 6
	AAX27204		306			200
	AAX27196	19	306	80.0		27
	AAX27193		306			26
	AAX27218		306			25
RpoB gene	AAX27212		306			24
Mycobacterium tube	AAC88922		87			23
M. tuberculosis	AAT12091		25			22
Propionibacterium	AAS59633		21500			2 2
Mycobacterium s	AAS99551		306			20
RpoB gene fragment	AAX27217		306			- L9
M. tuberculos	AAA89994		3853			18
Mycobacterium	AAA74651		3853			17
Mycobacterium	07	22	3534	100.0		16
Mycobacterium	AAH51976	22	3519			, L
Mycobacterium	967	17	970	•		1.4
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M.tuberculos	45	14	432	•		7.
Mycobacterium	95	24	306	•		- L
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ALIGNMENTS

RESULT AAT12092 ID AAT1

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AAT12092 standard; DNA; 20

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AAT12092;

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Antibiotic; resistance; spectrum; gene; mycobacterium; determination; amplification; tuberculosis; rpoB; fragiprimer; differential; hybridisation; pattern; rifampic rifabutin; species identification; ss. De Beenhouwer H, Jannes G, Rossau R; WPI; 1996-040250/04. 09-JUN-1995; (INNO-) INNOGENETICS NV. 09-JUN-1994; 14-DEC-1995. W09533851-A2 Synthetic M. tuberculosis rpoB gene fragment amplification primer 10-JUL-1996 (first entry) 94EP-0870093 95WO-EP02230 Machtelinckx L, Portaels F; rifampicin; fragment; P2

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TITLE
JOURNAL
REFERENCE
AUTHORS
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 3534)
Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M., picard, F.J. and Roy, P.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 3853)
Imboden,P., Troller,R., Marchesi,F., Telenti,A., Bodmer,T.,
Cole,S., Schopfer,K. and Burkart,T.
The rpoB gene of Mycobacterium tuberculosis
Unpublished
2 (bases 1 to 3853)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (11-JUL-1994) Paul Imboden, Institute for Medical Microbiology, University of Berne, Friedbuehlstrasse 51, Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Mycobacterium tuberculosis
Bacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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U12205
U12205.1 GI:51568
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3853 bp DNA linear BCT 02-MAR-2000
Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
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576. .>3853
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LVGTGNELRAALDAATSSSQESGVI EEVSADY I TVMHDNGTRRY RNHKFARSNHGTC
ANQCP I VDAGDRVEAGOVI ADGPCTDDGEMALGKNLL VA I HØMEGHRYEDA I ILS SRIL
VEEDVLTSI HI EEHE I DA DTK KLGAEEI TRD I EN I SDEVLADLDERG I VR I GA EVRDG
DILVGKUTPKGETELTPEERLLRAI FGEKAREVRDTSLKVPHGESGKVI GI RVYSRED
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I LIVGKYPRRANI GQ I LETHLGNGAHSGNK VDAAKGVPDWAARLPDELLEAQPNAI IVS
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FGFIETPYRKVVDGVVSDGIVYLTADEEDRHVVAQANSPIDADGRFVEERVLVRRKAG
        1173 c
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                               AX111339 3534 bp 1
Sequence 2072 from Patent W00123604
AX111339
                                                                                                                                                                                                                             l (bases 1 to 970)
Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T.
and Whelan,A.Christian.
Detection of a genetic locus encoding resistance
mycobacterial cultures and in clinical specimens
Patent: US 5643723-A 1 01-JUL-1997;
Location/Qualifiers
1. 970
                     AX111339.1
                                                                                                                                                                                                                                                                                                                                                                   Sequence 1 from I50706
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Sequence 59 from paten:
AR067448
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20; Conservative
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139 c 149 g
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Mycobacterium tuberculosis.

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Sequence 41
AR157042
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AR157007
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Kook, Y. and Kim,B.

Method for identifying mycobacterial sequence analysis of rpoB gene patent: US 6242584-A 7 05-JUN-2001;

Location/Qualifiers
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Sequence 7 from patent US
AR157008
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1 (bases 1 to 306)
1 (bases 1 to 306)
Kook, Y.-H. and Kim, B.-J.
Method for identifying mycobacterial species sequence analysis of rpoB gene patent: US 6242584-A 6 05-JUN-2001;
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                  LÖSSIO.1 GI:149991

RNA polymerase beta-subunit; rifampicin resistance.

Mycobacterium tuberculosis (strain H37) DNA.

Mycobacterium tuberculosis

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacteriumeae; Mycobacteriaceae;

Mycobacterium; Mycobacterium tuberculosis.complex.

1 (bases 1 to 432)

Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T.,
Colston,J., Matter,L., Schopfer,K. and Bodmer,T.

Detection of rifampicin-resistance mutation in Mycobacteriu
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Sequence
AR157051
                                                                                                                                                                      Mycobacterium tuberculosis RNA polymerase resistance gene, complete cds.
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Kook, Y. and Kim, B.

Method for identifying mycobacterial species sequence analysis of rpoB gene patent: US 6242584-A 41 05-JUN-2001; Location/Qualifiers 1. .306
                                                                                                                                                                                                                                                                                                                                ch 100.0%; l Similarity 100.0%; 20; Conservative
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Mycobacterium tuberculosis.

Mycobacterium tuberculosis

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;

Mycobacterium; Mycobacterium tuberculosis complex.
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Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 (bases 1 to 306) Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Kim,S.J., Kim,E.J. and Cha,C.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Korea
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1 (bases 1 to 306)
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/Codon_start=3
/Cransl_table=11
/product="RNA polymerase beta"
/product="RNA polymerase beta"
/protein_id="AAD55517.1"
/db_xref="GI:5902494"
/translation="RTVGELIONOIRVGMSRMERVVRERMTTODVEAITPQTLINIRP
VVAAIKEFFGTSOLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHPSH"
VVAAIKEFFGTSOLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHPSH"
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/strain="Tokyo T172"
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<1. .>306
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Pred. No. 4.6;
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                                          20;
                                                                                                                                                                         Kook, Y. and Kim, B. Kook, Y. and Kim, B. Method for identifying mycobacterial species sequence analysis of rpoB gene Patent: US 6242584-A 2 05-JUN-2001;
                                                                                                                                                                                                                                                               Unknown
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AR157003
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Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., K.Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
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Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)

J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

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/transl_table=11
/product="RNA polymerase beta"
/protein_id="AAD55518.1"
/db_xref="G1:5902496"
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VVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHPSH"
95 c 108 g 47 t
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/strain="H37Rv; ATCC27294"
/db_xref="ATCC:27294"
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Medicine, 28 Youngon-dong,
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Direct Submission
Submitted (06-APR-1998)
College of Medicine, 28
                                                                                                                                                                                                                      2 (bases 1 to 306)
Kook, Y.H., Kim, B.J.,
Kim, S.J., Chae, G.T.,
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AF057452
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Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
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Kook, Y. H., Kim, B.J., Lee, S.H.,
Kim, S.J., Chae, G.T., Kim, E.J. ε
Direct Submission
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157040 Sequenc	R1570	0	0	0		1	5
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57011 Sequenc	15701	σ,	0	0		: ن ـــ	
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057471 Mycobact	F05747	. ,_	· C	٠.		_ ،	Š
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57459 Mycoba	5745	Н	0	0.			6
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R157008 Sequenc	15700	6	0			N	æ
R157007 Sequenc	R15700	თ	0	Õ.	ш	N	7
R157003 Sequence	R15700	6	Ò			N	σ
F057454 Mycobact	F05745	ب	0	0	<u>, , , , , , , , , , , , , , , , , , , </u>	N	G
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F057451 Mycobact	05745	_	0	Ō	– ,	N	N
057450 Mycobac	5745	_	\circ	0		N	_

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ALIGNMENTS

REFERENCE AUTHORS REFERENCE AUTHORS KEYWORDS SOURCE ORGANISM ACCESSION VERSION RESULT AF057450 LOCUS DEFINITION JOURNAL MEDLINE TITLE PUBMED Lin. Microbiol. 37 (6), 1714-1720 (1999) Mycobacterium africanum.
Mycobacterium africanum
Mycobacteriam africanum
Bacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex. AF057450 306 bp DNA linear BCT 17-SEP-1: Mycobacterium africanum RNA polymerase beta (rpoB) gene, partial 2 (bases 1 to 306) Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., AF057450.1 GI:5902487 AF057450 10325313 BCT 17-SEP-1999

Result No.

Score

Query Match

Length DB

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Description

SUMMARIES

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SIFAAIGVVSGTQLDFCQSPRPVSVIHIHGTADPLVXYHGGPGAGEARIDGPPVPDLN
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                                                                                                                                                                                                                                                                                                                                                                                        Tuberculosis; disease diagnosis; oligonucleotide; DNA primer; polymerase chain reaction; DNA amplification; rpoB locus; TB;
                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                              15-OCT-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAT09676;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 620 BP; 103 A; 201 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            compared to the cleavage products of reference gene sequences method is used for detecting mutation in the human p53 gene; for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mutant sequences).
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                                                                                                                                                                                                                                                                                                                                                                   tuberculosis.
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                                /note= "M.
468..469
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                                                                                                                                                                 /note- "primer 354..373
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                     *tag=
                                                       '*tag-
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                                                                                                                                            KY290"
                                                                                                                                                                                                                                            DDIDH"
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0.0073;
hes 0;
                                          signature
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                         Query Match
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Matches 20
                                                                                       This oligonucleotide DNA primer is specific for Mycobacterium tuberculosis, and may be used to amplify a sample DNA by targeting a portion of the gene encoding rpoB. The 1st several bases comprise nonhybridizing tail consisting of filler bases followed by a restriction site incorporated to facilitate cloning using the amplicon at a later date, if desired. The remaining bases hybridize to bacterial rpoB DNA. The method provides for the detection of M. tuberculosis and the concurrent determination of its drug susceptibility, particularly to rifamycin. The method can provide often greater than 95% sensitivity and 100% specificity. The biological sample is a fluid or tissue sample from a human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             misc_feature
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                                                                       Sequence
                                                                                                                                                                                                       Disclosure; Fig.3; 54pp;
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                                                                                                                                                                                                                                                                                                    (MAYO-) MAYO
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tacggcgtttcgatgaaccc
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                                                                                                                                                                                                                        ion of Mycobacterium tuberculosis - by amplifying sample DNA primer set that targets portions of the gene encoding rpoB.
                                   Similarity
                                                                                                                                                                                                                                                                                                              HOFFMANN LA ROCHE INC
                                                                       970 BP; 182 A;
                         Conservative
                                                                                                                                                                                                                                                                                   Hunt JM,
                                                                                                                                                                                                                                                                                                      FOUNDATION.
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525..541
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/note= "primer!
952..966
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525
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640..666
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516
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952..966
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                           Mismatches
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No. 0.
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Matches 20
                                                                                                                                                                                                                                                                              method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of
                                                                                                                       1529
                                                                                                                                                                                                                                                                                                                                                              polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polypucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH51976;
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 24-JUL-2001
                            AAH02079;
                                                     AAH02079
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 68-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-329193/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-FEB-2000;
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                                                                                                                                                                                                                                           Sequence 3519
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les 20; Conserv
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                                                     standard;
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nilarity 100.0%;
Conservative 0
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(first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rotstein
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99US-0165124
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                                                   DNA; 3534 BP
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Pred. No. 0.0
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                                                                                                                                                                                  The present invention describes a method for generating a repertory of CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic cc acids of determined algal, archaeal, bacterial, fungal and parasitteal cspecies with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more cc used for producing probes and/or primers for detecting one or more cc used for producing probes and/or primers for detecting one or more cc used for producing probes and/or primers for detecting one or more cc used for producing probes and/or primers for detecting one or more cc detection and identification of an algal archaeal, bacterial, fungal and contained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the contained using the method of the invention can be used for the universal contained contained using the method of the invention can be used for the universal contained using the method of the invention can be used for the universal contained using the method of the invention can be used for the contained contained contained using the method of the invention of any bacterian of a therapeutic agent which is effective against the cross of the specific and contained using the method of the treptococcus phylum or group contained the detected include Abiotrophia adiacens, Bordetella sp., cc which can be detected include Abiotrophia adiacens, Bordetella sp., cc which accounts and coli, provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. Ca which are given in the exemplification of the present invention.
                                                                              Matches
                                                                                                  Query Match
Best Local
  1547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of algal, archaeal, bacterial, fungal and parasitical species in a test sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
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19-MAY-2000; 2000CA-2307010
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                                                                                                                                                                                                                           which are
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                   1 tacggcgtttcgatgaaccc
  TACGGCGTTTCGATGAACCC
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                                                                                20;
                                                                                                  Similarity
                                                                                                                                                                                  3534 BP;
                                                                                                                                                                                                                         given in the exemplification of the present invention.
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                                                                                Conservative
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Pred. No.
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                                                                                                                                                                                1188 G;
                                                                                               0.0064;
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AAA74651/c
ID AAA746
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AC AAA746
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RESULT 12
AAA89994/c
ID AAA89994;
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AC AAA89994;
XT
DT 18-DEC-2000 (first
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DE M. tuberculosis rpoB
XX
C Drug resistance; rif
KW RNA polymerase beta
XX
OS Mycobacterium tuberc
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Best Local Similarity 100.
Matches 20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence is the rpoB gene from Mycobacterium tuberculosis. Alfampin resistance is largely associated with point mutations localised in a small core region of 81 base pairs in the rpoB gene, which encodes the RNA polymerase beta subunit. To detect a mutation, a complex is formed comprising a first sequence representing the predetermined region of the gene of the organism and a second sequence representing the corresponding region of the gene of the wild type organism in double stranded form. Each member of at least one pair of non-complementary strands within the complex has a label. The association of the labels in the complex is related to the presence of the mutation. The presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2122
                                     Mycobacterium tuberculosis
                                                                                          RNA polymerase beta subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-JAN-1999;
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                                                                                                                 Drug resistance; rifampin; rifampicin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method for detecting drug resistance in a strain of an organism, particularly for detecting rifampin resistance in Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (DADE-) DADE BEHRING INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis rpoB gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 tacggcgtttcgatgaaccc 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TACGGCGTTTCGATGAACCC 2103
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fig
                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is related to the drug resistance of the strain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0233996
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                                                                                                                                                                           rpoB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       723 A; 1173 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                DNA;
                                                                                                                                                                     gene encoding RNA
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); Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1293 G;
                                                                                                                                                                        polymerase beta subunit.
                                                                                                                 pyrazinamide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
0.0064;
hes 0;
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RESULT 1
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Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This invention relates to a method for detecting drug resistance in a strain of an organism. The method comprises detecting the presence of a least 1 mutation in a first sequence and relating the presence of the mutation to drug resistance. Included in the invention are a kit for carrying out the method and a method for detecting the presence of a difference between two related nucleic acid sequences in an organism. The methods are useful for detecting resistance to drugs such rifampin and pyrazinamide in Mycobacterium. The present sequence represents the Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase beta subunit). The sequence is used in an example of the method of the invention for the detection of rifampin resistance in M. tuberculosis.
De Beenhouwer H,
                                                                                                                                                                                                                           M. tuberculosis rpoB gene fragment amplification
                                                                                                                                                                                                                                                                                                                                                            2122 TACGGCGTTTCGATGAACCC 2103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Detecting resistance of drugs such as rifampicin Mycobacterium, comprising detecting mutations in them to drug resistance -
                       (INNO-) INNOGENETICS NV
                                                                     09-JUN-1995;
                                                                                                                   W09533851-A2
                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                           AAT12096;
                                                                                                                                                                                                                                                                                                  AAT12096 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3853 BP; 723 A;
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22-APR-1999;
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                                                                                            14-DEC-1995
                                                                                                                                                                                         determination;
                                                                                                                                                                                                  Antibiotic; resistance; spectrum; gene; mycobacterium;
                                                                                                                                                                                                                                                    10-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Liu YP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DADE-) DADE BEHRING INC
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                                                                                                                                                                              differential;
                                                                                                                                                                  species
                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                  (first entry)
                                               94EP-0870093
                                                                                                                                                                                         amplification;
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                                                                     95WO-EP02230
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99US-0296894
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Jannes
                                                                                                                                                                                                                                                                                                  DNA;
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                                                                                                                                                                            hybridisation; pattern;
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Pred. No.
Machtelinckx
                                                                                                                                                                                       tuberculosis; rpoB;
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Portaels
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a gene and
                                                                                                                                                                                                                           primer
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relating
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Best Loc
Matches
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This oligonucleotide DNA primer is specific for Mycobacterium tuberculosis, and may be used to amplify a sample DNA by targeting a portion of the gene encoding rpoB. The method provides for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Probes and primers for determn. of antibiotic resistance spectrum of Mycobacterium, opt. coupled with species identification – from different patterns of hybridisation with rpoB gene
                                                                    with a primer
                                                                                                      WPI; 1996-030581/03
                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                               Mycobacter1um
                                                                                                                                                                                                                                                                                                                                                                                                                 AAT09670 standard; DNA;
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                                                                                                                            Felmlee TA,
Young KKY;
                                                                                                                                                             (HOFF ) HOFFMANN LA ROCHE (MAYO-) MAYO FOUNDATION.
                                                                                                                                                                                               26-MAY-1994;
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                                                                                                                                                                                                                                                                 WO9533074-A1
                                                                                                                                                                                                                                                                                                                        Tuberculosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
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les 19; Conserv
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                                             Page
                                                                    of Mycobacterium tuberculosis imer set that targets portions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 39;
                                                                                                                                                                                                                                                                                                             chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP; 4 A; 5 C;
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                      Hunt JM,
                                              39;
                                                                                                                                                                                                                                                                                                            disease diagnosis;
in reaction; DNA an
                                                                                                                                                                                                                                                                                                                                              tuberculosis
                                                                                                                                                                                               94US-0250030
                                                                                                                                                                                                                    95WO-US06790
                                             54pp;
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                                             English
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Pred. No.
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amplification; rpor
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                                                                                                                                      Roberts GD,
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0.038;
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f the gene enc
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                                                                                                                                       Whelen
                                                                                                                                                                                                                                                                                                             DNA primer;
B locus; TB;
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                                                                   ying sample DNA encoding rpoB.
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                                                                                                                                                                                                                                                                                                             PCR;
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RESULT 15
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                                                                                                                                                                                             17-SEP-1992;
30-APR-1992;
14-AUG-1992;
16-APR-1993;
PCR amplification was used to obtain rpoB genes from rifampicin-resistant Mycobacterium leprae strains. A comparison with the sequence of the rpoB gene from sensitive strains (AQAG5132) revealed mutations in the region encoding amino acids 400-450. A common
                                                        Rapid detection of antibiotic resistance in Mycobacteria isoniazid, rifampicin or streptomycin resistance in tubes by detecting mutation in katG, rpoB or rpsL genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection of M. tuberculosis and the concurrent determination of
drug susceptibility, particularly to rifamycin. The method can
provide often greater than 95% sensitivity and 100% specificity.
The biological sample is a fluid or tissue sample from a human.
                                                                                                                                                            (ASSI-)
(INSP)
(MEDI-)
                                                                                                                                                                                                                                                                                                                                  Key
                                         Example
                                                                                           P-PSDB;
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                                                                                                                                                                                                                                                                                                                                                         Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                          mutant;
                                                                                                                                                                                                                                                                                                                                                                                  rifampicin;
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DB; AAR43671.
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                                                                                                                                                             MEDICAL RES COUNCIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                   Zhang
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                                                                                                                           Cole
                                                                                                                                                                                                                                                                                                                                                                                  antibiotic;
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92US-0875940.
92US-0929206.
93FR-0004545.
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/note=
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                                        97pp;
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strains the Ser codon
nucleotides 1273-1275)
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CC mutation seen in resistant strains occurs at codon 425 where Ser is Substituted, most frequently by Leu.

XX Sequence 3447 BP; 667 A; 965 C; 113 G; 656 T; 0 other:

Ouery Match

Best Local Similarity 100.0%, Score 14; DB 14; Length 3447;

Hatches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

7 gtttcgstgaaccc 20

Db 1448 GTTTCGATGAACCC 1435

Search completed: August 8, 2002, 00:01:26

Job Lime: 7615 sec
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Result
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Maximum DB
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Perfect score:
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                                                                                                                                                                                           Score
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Match Length C
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20
1 tacggcgtttcgat
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OLIGO_NUC Gapext 60.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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      W06754 SMEST0390 S
T24127 SMEST0325 S
BEB96357 601439015
BM077908 pb21906.y
AW694629 NF078E03S
AL482362 T. bruce1
AQ783856 HS_2001_A
AL466454 T. bruce1
BH615799 BMBAC304F
BE053145 GA_EA000
AL269530 Tetracdon
BM007170 603614933
AV640031
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AV640075 BB177553
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AQ660540 Sheared D
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RESULT 1 W06754/c LOCUS DEFINITION		C 45	C 44	43	4 4 7 -	c 40	39			c 36		34			c 31			28		c 26			23	22	21	20	19	c 18	
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W06754 W06754 SMEST0390 Schistosoma mansoni, adult worm, (schistosoma mansoni, adult worm, (schistosoma mansoni onna cuperz 3 % es	ALIGNMENTS				10 BF2/01/6	В			×		ъ				9 AV642141			9 AW618736			>			Þ			9 AJ284239		
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		FEATURES Source				TITLE JOURNAL COMMENT	AUTHORS	ORGANISM	KEYWORDS SOURCE	LOCUS DEFINITION ACCESSION
/rab_nost="thiob, JMI09" /note="Vector: BA vector; Site_1: NotI; Site_2: HindIII; /note="Vector: NA from male and female adult worms was Total cellular RNA from male and female adult worms was extracted according to a modification (Pulssant, C. and Houdebine, L. M. BioFeedback B, 148-149, 1990) of the Guanidine Thiocyanate procedure (Chomczynski, P. and	/strain="NMRI" /db_xref="taxon:6183" /clone="Schistosoma mansoni, adult worm, Gloria Franco" /lab bot and mansoni, adult worm, Gloria franco"	Location/Qualifiers 1234 /organism="Schistosoma mansoni"	Fat: (553)4414001 Fat: (5531)441409 Email: gfranco@mono.icb.ufmg.br Seg primer: M13 Forward	Gerais Avenida Antonio Carlos 6627, Belo Horizonte, MG, Brazil, 31270-010	Laboratorio de Genetica-Bioquimica, Departamento de Bioquimicae Imunologia Instituto de Ciencias Biologicas. Universidade Federal de Minas	Tranco, G.K. and rena, S.D.J., Unpublished Unpublished (1996) Contact: Franco G.R. and Pena S.D.J.		Schistosoma mansoni Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma.	EST. Schistosoma mansoni.	

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BASE COUNT
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Best Local S
Matches 17
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les 17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: (5531)4415611
Fax: (5531)4415409
Email: gfranco@mono
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T24127 579 bp mRNA SMEST0325 Schistosoma mansoni, adult worm, Schistosoma mansoni cDNA clone SMPBC65 3',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   using a directional cDNA
Gene 152, 141-147 (1995)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gerais
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Identification of new Schistosoma mansoni genes by the EST strategy
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primer: M13 Forward.
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/lab_host="DH10B, JM109"
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/lab_host="DH10B, JM109"
/note="Vector: BA vector; Site_1: NotI; Site_2: HindIII;
/note="Vector: RNA from male and female adult worms was
extracted according to a modification (Puissant, C. and
Houdebine, L. M. BioFeedback 8, 148-149, 1990) of the
Guanidine Thiocyanate procedure (Chomczynski, P. and
Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+
RNA was purified by oligo dT column and cDNA was
synthesized as described previously (Adams, M. D. et al.
Nature Genet. 4, 373-389, 1993). cDNA was ligated to a
                                                                                                                                                                                                                                                                                  Franco
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                                                                                                                                                                                                                                                                                                              /clone
                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:6183"
/clone="SMPBC65"
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2.2;
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, Gloria Franco
, mRNA sequence.
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FEATURES

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5 gcgtttcgatgaaccc 20

Matches

16;

Conservative

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Mismatches

Indels

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0

COMMENT

REFERENCE

AUTHORS

TITLE

JOURNAL

VERSION KEYWORDS

ACCESSION

SOURCE

RESULT T24127/c

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ORGANISM
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 Query Match
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|75 TACGGCGTTTCGATGAA 59
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: ggapbs-r@mail.nih.gov
Tissue Procurement: ATCC//CTD//DTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 624)
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA sequence.
BE896357
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Robert
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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                                                                                              മ
                                                                                                           /db_xref="taxon:9606"
/clone="IMAGE:3924266"
/clone_lib="NIH_MGC_72"
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pcMV-SPPRT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo (Average insert size 2 kb. Library constructed by Life Technologies."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        two fold molar excess of a NotI/HindIII digested plasmid DNA (lafmid BA vector, a phagemid derived from pEMBL, Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and electroporated into E. coli strain DH10B (BRL). The library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel, containing the smear of the library and electroporation into DH10B cells. "
                                                                                          Technologies.
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80.0%;
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100.0%;
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Pred. No.
 Score 16;
Pred. No.
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DB
10;
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2.4;
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                   Length 624;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The library was constructed by Claire Murphy, Brandi Chiapelli, Dr. James McCarter at Washington University, St. Louis. DNA Sequencing by: Washington University Genome Sequencing Center. Location/Qualifiers
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Email: est@watson.wustl.edu
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314 286 1810
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/db_xref="taxon:29170"
/clone_lib="Ancylostoma caninum L3
Chiapelli McCarter"
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/lab_host="DH10B"
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Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
The Sam
                                                                                                                                                            Direct Submission
Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hi Cambridge CB10 1SA, E-mail: barrell@sanger.ac.uk and
                                                                                                                                                                                                                                                                                         Hall,N., Bowman,S., Lennard,N.J., Do
Chillingworth,C., Ormond,D., Harris,
Melville,S.E., Rajandream,M.A. and E
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Insert Length: 736 Std Error: 0.0
Plate: 078 row: E column: 03
Seg primer: TCACACAGGAAACAGCTATGAC.
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He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Be.,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon,R.A.
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Trypanosoma brucei (TREU927/4 GUTat to give a tight size distribution (
                                                                 Rockville, MD. Genomic DNA isolated
                                                                                             Constructed at the Institute for Genomic Research (TIGR),
                                                                                                                                   nhl@sanger.ac.uk
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/clone_lib="Developing stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a
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/db_xref="taxon:3880"
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C., Ormond,D., Harris,B., El-Sayed,N.,
Rajandream,M.A. and Barrell,B.G.
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                                                                                                                                                                                                                                                             401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 2001 row: K column: 18
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                                                                                                                                                                                    High quality sequence stop: 536
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Seq primer: T7
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High Throughput Sequencing Center
University of Washington
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Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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AQ783856.1 GI:5691480
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Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
Location/Qualifiers
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                               /note="Organ: sperm; Vector:
E-Coli DH10B"
                                                                                                        /db_xref="taxon:9606"
/clone="Plate=2001 Col=18 Row=K"
                                                                       /sex≃"male"
                                                                                                                                              /organism="Homo sapiens"
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="247h04"
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Constructed at the Institute for Genomic Research (TIGR),

Rockville, MD. Genomic DNA isolated from a cloned population of

Trypanosoma brucei (TREU927/4 GUTat 10.1) was mechanically shear

to give a tight size distribution (
4 kb). The v + 1 method used for the library construction is

described in detail in Smith, H. and Venter, J.C. (Making small

Insert libraries for whole genome shotgun sequencing projects.

Genome Sequencing: A Practical Approach, eds. M. Vaudin and B.
Trypanosoma brucei
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
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                               Trypanosoma brucei.
                                                                  AL477985.1
                                                                                   AL477985
                                                                                             genomic survey sequence
                                                                                                            T. brucei sheared genomic DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-DEC-2000) Trypanosoma brucei genome sequencing project, Sanger Centre, The Wellcome Trust Genome Campus, Hi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hall,N., Bowman,S., Lennard,N.J., Doggett,J., Atkin,R., Chillingworth,C., Ormond,D., Harris,B., El-Sayed,N., Hou,L., Melville,S.E., Rajandream,M.A. and Barrell,B.G.
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T. brucei sheared genomic DNA clone
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Trypanosoma brucei
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15; Conservative
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/strain="TRED927"
/db_xref="taxon:5691"
/clone="140903"
/clone="140903"
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Onchocercidae; Brugia.
1 (bases 1 to 631)
1 (bases 1 to 631)
Whitton,C., Daub,J., Ware,J., Quail,M., Hall,N.,
,J., Guillano,D., Slatko,B. and Blaxter,M.
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Hall, N., Bowman, S., Lennard, N.J., Doggett, J., Atkin, R.,
Chillingworth, C., Ormond, D., Harris, B., El-Sayed, N., Hou, L.,
Melville, S.E., Rajandream, M.A. and Barrell, B.G.
Direct Submission
                                                  Email: mark.blaxter@ed.ac.uk
Sequenced from the Brugia malayi BAC library constructed by Claire
Whitton and Dr Mike Quail. The sequence was generated by The
Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
collaboration with Mark Blaxter, ICAPB, University of Edinburgh,
                                                                                                                                                         3JT, UK
Tel: +44 131 650 6760
Fax: +44 131 670 5450
                                                                                                                                                                                                              Contact: Blaxter ML
Institute of Cell, Animal and Population Biology
University of Edinburgh
Ashworth Labs, King's Buildings, West Mains Road,
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BH615799
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BMBAC304F01SP6_PSU Brugia malayi
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Details of T. brucei sequencing at the Sanger Centre are available at http://www.sanger.ac.uk/Projects/T_brucei/.
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Constructed at the Institute for Genomic Research (TIGR),
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                  Edinburgh, UK.
Seq primer: SP
                                                                                                                                                                                                                                                                                                      Unpublished (2000)
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/strain="TREU927"
/db_xref="taxon:5691"
/clone="190a10"
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                                                                                                                                                                                                                                                                      Clemson, SC 29034, 100 Jordan Hall, Člemson, SC 29034, Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Seq primer: TAATACGACTCACTATAGGG
Seq primer: TAATACGACTCACTATAGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACGGCGTTTCGATGA 620
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BE053145
BE053145.2 GI:13244065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gossypium arboreum
Gossypium arboreum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                 Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           An integrated analys of the cotton fiber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.
An integrated analysis of the genetics, development, and evolution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000 on Jun 8, 2000 th
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gossypium arboreum.
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/note="Vector: pBACe3.6; Site_1: BamH I; Brugia malayi
genomic DNA was partially cleaved with Sau3A I and size
fractionated. 7,392 clones were generated with mean insert
size -48 kbp. The library was constructed by Claire
whitton, Blaxter Nematode Genetics Lab, University of
Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
Unit, The Sanger Centre, Cambridge, UK."
                                                                    /clone="GA_Ea0002K16f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10 dpa"
/lab_host="E. coli"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
| 132 c 151 g 236 t 2 others
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/strain="TRS"
                                                                                                                                                                        /cultivar="8400"
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/tissue_type="whole parasite"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="Brugia malayi Genomic Bac Library
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mRNA sequence.
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603614933T1 NIH_MGC_110
                                                                                                                                                                                 l Similarity
15; Conserv
                                                                                                                                                                                                                                                                                                                                                                           Submitted (12-APR-2000) to the EMBL/GenBank/DDBJ databases This sequence is a single read and was generated as part of a lascale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottler,P., Quetier,F., Saurin,W. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodon.

1 (bases 1 to 1033)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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/note="Genoscope :
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/db_xxef="taxon:99883"
/clone="073004"
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42;
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                                                                                                        Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K., Nakamura, Y. and Tabata, S.

Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii

DEAR. Res. 7 (5), 305-307 (2000)
                                                                                                                                                                                                                                                                               Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Eukaryota, Viridiplantae; Chlorophyta; Chlorophyceae;
Chlamydomonadaceae; Chlamydomonas.
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15; Conserv
Contact: Erika Asamizu
The First Laboratory for Plan
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AV640031 Chlamydomonas reinhardtii 5% CO2 Chlamydomonas cDNA clone HCL009b04_r 5', mRNA sequence.
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Tissue Procurement: ATCC
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1 (bases 1 to 1218)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jnpublished (1999)
                                                                                                                                                                                                                                                          (bases 1 to 247)
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Location/Qualifiers
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/clone_lib="NIH_MGC_110"
/tissue_type="ductal carcinoma, cell line"
/tab_host="Diflow (phage-resistant)"
/note="organ; pancreas; vector: pOTB7; Site_1: XhoI;
Site_2: EcoRI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

70 a 446 c 244 g 154 t 4 others
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/db_xref="taxon:9606"
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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 254
                   4 ggcgtttcgatgaa 17
GGCGTTTCGATGAA 241
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Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                              The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20539644
Contact: Erika Asamizu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Asamizu, E., Miura, K., Kucho, K., Inoue, Y., Fukuzawa, H., Ohyama, K., Nakamura, Y. and Tabata, S.
Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Similarity 100.0%;
14; Conservative (
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/note="Vector: pBluescriptII SK-; Site_l: EcoRI; Site_2:
xhoI; The cDNA library was constructed from cells cultured
in a medium with bubbling air containing 5% carbon
dioxide"
a 85 c 60 g 59 t
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79 c 54 g 53 t
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/db_xref="taxon:3055"
/clone="HCL009b04_r"
/clone_1ib="Chlamydomonas reinhardtii 5% CO2"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
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/db_xref-"taxon:3055"
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                                                                                       70.0%; Score 14; 100.0%; Pred. No.
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Mismatches 0;
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Search completed: August 7, 2002, 23:12:33 Job time: 11072 sec

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Maximum Match 100%
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Maximum DB seq length: 2000000000
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/2/ina/FCTUS_COMB.seq:*

5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*
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Copyright (c) 1993 - 2000 Compugen
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US-08-250-030-9

PCT-US-5-06790-9

US-09-372-442A-3

US-09-372-448A-5

US-08-674-887A-5

US-08-951-844-5

US-08-292-498A-59

PCT-US-5-10813-59

US-09-372-422A-47
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Sequence 59, Appl Sequence 135, App Sequence 136, App Sequence 137, App Sequence 139, App Sequence 140, App Sequence 140, App Sequence 1, Appli Sequence 1, Appli Sequence 71, Appli Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 3, Appli Sequence 5, Appli Sequence 6, Appli 6,
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RESULT 1 US-08-313-1 Sequence Patent NG GENERAL APPLIC COMPUT MEDJ COMPUT MEDJ COMPUT AMEDJ COMPU	00000000000000000000000000000000000000
85-59/c 59, Appl 58, Appl 58, Appl 60, S8176 1 NFORMAL ANT: CC ANT: CC ANT: CC ANT: TC	13.8 69.0 13.8 69.0 13.8 69.0 13.8 69.0 13.8 69.0 13.8 69.0 13.6 68.0 13.6 68.0 13.6 68.0 13.6 68.0
	1176 4 1176 4 1176 4 1375 4 1485 4 12394 3 2394 4 17612 4 4403765 4 686 4 699 4 1099 4 1209 1
85 ction of Antibiotic terium Tuberculosis on, Farabow, Garrett 1.0, Version #1.25 3,185 56.0068-00000	US-08-911-853-34 US-09-479-409-34 US-09-479-453-34 US-09-372-422A-39 US-09-372-064-1 US-09-271-815-1 US-09-271-815-1 US-09-271-815-1 US-09-479-453-29 US-09-479-453-29 US-09-479-453-29 US-09-404-671-3 US-09-404-671-3 US-09-372-422A-45 US-09-372-422A-79 US-09-374-309A-5 US-08-314-309A-2
Resistance	Sequence 34, Appl Sequence 34, Appl Sequence 37, Appl Sequence 37, Appl Sequence 1, Appli Sequence 1, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 3, Appli Sequence 45, Appli Sequence 705, App Sequence 705, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 29, Appli Sequence 7, Appli Sequence 29, Appli

Query Match

100.0%;

Score 20;

DB 2;

Length 432;

Best Local Similarity 100. Matches 20; Conservative

100.0%;

Pred. No. 0.033;

Mismatches

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RESULT 3
US-08-757-653-135/c
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US-09-082-614A-59/c
Sequence 135, Application US/08757653 Patent No. 5843669
                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 59,
                                                                                                                                                                                                                                                                                                   TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodner, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCE: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                        428 TACGGCGTTTCGATGAACCC 409
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                                                                                                                1 tacggcgtttcgatgaaccc 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C
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E: Dunner
1300 I Street, N.W.
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Zhang, Ying
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                                                                                                                                                                     APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
CORRESPONDENCE ADDRESS:
ADDRESSE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CCITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 136, Application US/08757653 Patent No. 5843669
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INFORMATION FOR SEQ ID NO:
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                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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LENGTH: 620 base pairs
TYPE: nucleic acid
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kaiser, Michael W. APPLICANT: Lyamichev, Victor I. APPLICANT: Lyamichev, Natasha
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296 TACGGCGTTTCGATGAACCC 277
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Cleavage Of Nucleic Acid Using TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                                                                           COUNTRY:
                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity 100 nes 20; Conservative
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STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Ingolia, Diane E. REGISTRATION NUMBER: 4(
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115) 397-8338
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Pred. No.
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; MOLECULE TYPE:
US-08-757-653-136
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US-08-757-653-137/c
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US-08-757-653-137
                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FORS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8310
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 137:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 5843669
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Best Local Similarity
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TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 136
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: FOI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT
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FILING DATE:
CLASSIFICATION: 435
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STATE: California
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                              TOPOLOGY:
                                            STRANDEDNESS:
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                                                         nucleic acid
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1: DNA (genomic)
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Pred. No. 0.034;
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                                                                                                  Patent No. GENERAL II
                                                                                                                 Sequence 139, Application US/08757653 Patent No. 5843669
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Best Local :
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TELEFAX: (415) 397-83
INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kaiser, Michey, Victor I.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
TITLE OF SEOUENCES: 190
            APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: FO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS: single
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                                                                                                  INFORMATION:
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5843669
                                                                                                                                                                                                                                                                                                 h 100.0%; Score 20; DB 2;
Similarity 100.0%; Pred. No. 0.034;
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                                                                                                                                                                                                                                                                                   Conservative
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CORRESPONDENCE ADDRESS:

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE,DOCKET NUMBER: FORS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8310
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 139:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/757,653
                                                                                                                                                                                      ZIP: 9410*
COMPUTER READABLE FORM:
"TYPE: Floppy disk
                           ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            325 TACGGCGTTTCGATGAACCC 344
REFERENCE/DOCKET NUMBER:
                   REGISTRATION NUMBER:
                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                           ADDRESSEE: Medien v Canal STREET: 220 Montgomery Street,
                                                                                             FILING DATE:
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TOPOLOGY: linear
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/757,653
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o. 5843669
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                 40,027
FORS-02565
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Pred. No. 0.034;
D; Mismatches
                                                                                                                                                                                                                                                                                                             Suite 2200
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RESULT 9
US-08-797-812-24/c
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                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/797,812
FILING DATE: 07-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,765
FILING DATE: 15-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2. Patent No.
                                                                                                                                                                                  FILING DATE: 15-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/629,031
FILING DATE: 08-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,631
FILING DATE: 01-MAR-1996
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Best Local
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LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (415) 397-83 INFORMATION FOR SEQ ID NO:
              REGISTRATION NUMBER: 35,136
REFERENCE/DOCKET NUMBER: 16:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2420
TELEFAX: 415-326-2422
                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 61
FILING DATE: 08-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Fitts, Renee A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Wang, Ching
TITLE OF INVENTION: Chip-Based Species Identification and
TITLE OF INVENTION: Phenotypic Characterization of Microorganisms
NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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TELEPHONE: (415) 705-8410
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                                                                                 NAME: Fitts, Renee A. REGISTRATION NUMBER:
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CA
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Chee, Mark S.
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SEQ ID NO:
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415) 397-8338
SEQ ID NO: 140:
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Pred. No. 0.034;
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SEQUENCE CHARACTERISTICS:

GENERAL INFORMATION:

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RESULT 11
PCT-US95-06790-1/c
; Sequence 1, Application PC/TUS9506790
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                                                                                                                                                    Query Match
Best Local Similarity
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Best Local Similarity
                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                       TELEFAX: 612-339-3061 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Persing,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,030
FILING DATE: 26-MAY-1994
                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                 MOLECULE TY
                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION: TELEPHONE: 612-339-0331
                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                              332 TACGGCGTTTCGATGAACCC 313
                                                                                                                                                                                                                                                           TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UZIP: 55402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS: $1
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 tacggcgtttcgatgaaccc 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Minneapolis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              nucleic acid
                                                                                                                                                                                                                                 TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ×
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Schwegman, Lundberg & Woessner 3500 IDS Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Persing,
                                                                                                                                      100.0%; silarity 100.0%; sometive 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Clinical Specimens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                David H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Detection of a Genetic Locus Encoding Resistance to Rifampin in Mycobacterial Cultures and
                                                                               652
                                                                                                                                                                                                                                                                                                                                                                                  150.105US1
                                                                                                                                                       Score 20;
Pred. No.
                                                                                                                                        Mismatches
                                                                                                                                                    0.036;
                                                                                                                                                                     DB 1;
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                                                                                                                                                                    Length 970;
                                                                                                                                      Indels
                                                                                                                                      0;
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                                                                                                                                      Gaps
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PCT-US95-06790-1
                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 71,
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                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                  APPLICANT: DE BEENHOUTE...

APPLICANT: PORTAELS, FRAN OISE
APPLICANT: MACHTELINCKX, LIEVE
APPLICANT: MACHTELINCKX, LIEVE
APPLICANT: JANNES, GEERT
APPLICANT: JANNES, GEERT
APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: METHOD FOR DETECTION OF THE ANTIBIOTIC
TITLE OF INVENTION: RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
TITLE OF SEQUENCES: 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 612-339-03:
TELEFAX: 612-339-3061
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Reasch, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 150
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Schwegman, Lundberg & Woessner
STREET: 3500 IDS Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Mayo Foundation for Medical Education and Resea
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                          CITY: WASHINGTON STATE: D.C.
                                                                                                                                                                                 ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & STREET: 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 2 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                          COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 tacggcgtttcgatgaaccc 20
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                                                                                                         20005-3934
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 20; DB 5;
Pred. No. 0.036;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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RESULT 13
US-08-313-185-57/c
; Sequence 57, Application US/08313185
natent No. 5851763
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Best Local Similarity 100.0%; Pred. No.
Matches 19; Conservative 0; Mismatc
                                       TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: 57:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION UNMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
CCASSIFICATION: 435
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
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TELEFAX: 202-371-2540
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APPLICATION NUMBER: US
                                                                            TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
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TOPOLOGY: linear
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REFERENCE/DOCKET NUMBER: 1657.0010000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: GOLDSTEIN, JORGE A. REGISTRATION NUMBER: 29,0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 21
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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1300 I Street, N.W
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                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                            (202) 408-4000
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; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-09-082-614A-57
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US-09-082-614A-57/c
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    Matches
                Query Match
Best Local Similarity
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Best Local :
                                                                                                                                                                      TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
PAPELICATION NUMBER: US 0
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/082,614
                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 1300 I S:
CITY: Washington
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                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE: D.C
                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
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Local Similarity 95.0%;
les 19; Conservation
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                                                                                                                                                              LENGTH:
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                                                                                                                                           nucleic acid
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                                                                                                                                                          3447 base pairs
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   Conservative
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Zhang, Ying
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                                                                                                                            single
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              92.0%; Score 18.4; DB 95.0%; Pred. No. 0.32;
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Mismatches
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                             DB 3; Length 3447;
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1454 TACGGTGTTTCGATGAACCC 1435

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STATE: VA

STATE: VA

COUNTRY: US

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/08/622,354

FILING DATE: 27-MAR-1996

CLASSIFICATION ** 435
ATTORNEY/AGENT INFORMATION:

NAME: Price, Robert L.

REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 434-061

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 684-1111

TELEFAX: (703) 684-1114

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1472 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cONA
HYPOTHETICAL: NO
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US-08-622-354-2/c
Sequence 2, Application US/08622354
; Sequence 2, Application US/08622354
; Patent NO. 5827518
; Patent NO. 5827518
; APPLICANT: WEBB, Bruce A.
; APPLICANT: CUI, Liwang
; TITLE OF INVENTION: VIRAL AND INSECT GENES THAT INHIBIT THE
; TITLE OF INVENTION: IMMUNE SYSTEM AND METHODS OF USE THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
ADDRESSEE: LOWE ABSTOR LERITANC & RECKED
                                                                                                              ₽
                                                                                                                                                                                                                                                                                                                  ; NAME/KEY:
; LOCATION:
US-08-622-354-2
Search completed: August 7, 2002, 21:54:25 Job time: 24020 sec
                                                                                                                                                                                                   Query Match 79.0%; Score 15.8; I Best Local Similarity 89.5%; Pred. No. 8; Matches 17; Conservative 0; Mismatches
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1105 TACGGGGTTTAGATGAACC 1087
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Listing first 45 summaries
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BF220419 NXCI_146
BF169611 NXCI_125
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AA556698 553 Loblo
BF777209 NXSI_066
W06754 SMEST0390 S
T24127 SMEST0325 S
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BF25221 EST420184
'BE896357 601439015
'BH615799 BMBAC304F
A6141490 Pan trogl
AW064407 Sp0996 KR
JAL147937 Anopheles
BG908684 TaLr1170D
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BB501888 BB501888	BF953380 RC3-NN019	AZ577000 06d05 Sho	EBpi05	BM096759 EBma07_SQ	ď	AV631818	HS_5197	AQ783856 HS_2001_A	BI506216 BB170018A	AV642766 AV642766	_	AV642711 AV642711	AV643117 AV643117	AW618736 EST320722	AV396989 AV396989	AL242176 Tetraodon	AV644609 AV644609	вм077908 рb21g06.у	AV640876 AV640876	BG140300 EST480742	AL147715 Anopheles	BI663170 603286791	AL320465 Tetraodon	BF204833 601867133	AL189251 Tetraodon	AZ125549 OSJNBb009	AL229661 Tetraodon

ALIGNMENTS

	FEATURES source	REFERENCE AUTHORS TITLE JOURNAL COMMENT	RESULT 1 BF220419 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM
/organism="Pinus taeda" /organism="Coastal plain loblolly pine from North Carolina" /db_xref="Coastal plain loblolly pine from North Carolina" /db_xref="Laxon:3352" /clone="NXCI_146_A06" /clone="INXCI_CNST Xylem Compression wood Inclined)" /tissue_type="Yylem" /cell_type="Compression" /dev_stage="Juvenile" /lab_host="Xil-Blue" /lab_host="Xil-Blue" /note="Vector: BlueScript SK; Site_1: Eco RI; Site_2: XhoI : The library is from early (spring) wood, taken from three six-year old trees (three different genotypes), in the juvenile phase. These trees were induced to form compression wood by bending to a 45 degree angle and tying them to the ground. Differentiating xylem was harvested from the bottoms of the inclined stems, and a mixture of	Tel: 919 515 7800 Fax: 919 515 7801 Email: ajohnson@unity.ncsu.edu Seq primer: T3. Location/Qualifiers 1396	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 396) Sederoff, R. Molecular Basis of Wood Formation in the Pine Megagenome Unpublished (2000) Contact: Johnson, Arthur North Carolina State University	BF220419 WXCI_146_A06_F NXCI (Nsf Xylem Compression wood Inclined) Pinus taeda cDNA clone NXCI_146_A06 5', mRNA sequence. BF220419 BF220419.1 GI:11126551 EST. Lobiolly pine. Pinus taeda

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KEYWORDS
SOURCE
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North Carolina State University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 399)
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NXCI_125_C05_F NXCI (Nsf Xylem Compression wood Inclined) Pinus
taeda cDNA clone NXCI_125_C05 5', mRNA sequence.
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primer: T3.
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a 84 c 122 g 110 t 9 others
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North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
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/cell_type="Side"
/dev_stage="Juvenile"
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/strain="Coastal plain loblolly pine
/db_xref="taxon:3352"
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                                                                                                                      Fax: 919 515 7801
Email: ajohnson@unity.ncsu.edu
Seq primer: T3.
Seq primer: Ton/Onalifiers
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dept. of Forestry, NC, 27695-8008
                                                                                                                                                                         Unpublished (2000)
Contact: Johnson, Arthur
Contact: Johnson, Arthur
North Carolina State University
Tel: 919 515 7800
Fax: 919 515 7801
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                                                                                                                                                                                                                                                                   Molecular Basis of Wood Formation in the Pine Megagenome
                                                                                                                                                                                                                                                                                       Sederoff, R.
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Forest Biotechnology Group
North Carolina State University
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note-"Vector: lambda-ZAP; Site_1: EcoRI; Site_2: XhoI; The result of subtraction of C library with N library. Immature xylem from the underside of inclined stems of differentiating compression wood was subtracted with immature xylem from the side of inclined stems of differentiating wood. A mixture of four genotypes were used. Oligo-dT primed cDNA was directionally cloned into the EcoRI-XhoI lambda-ZAP vector arms."
/strain="coastal plain loblolly pine from North (/db_xref="taxon:3352" /clone="NXSI_066_E05" /clone_11b="NXSI (Nsf Xylem Side wood Inclined)"
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/db_xref="taxon:3352"
/clone="1CAB4G"
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/tissue_type="Xylem"
/lab_host="SOLR"
                                                                            /organism-"Pinus taeda"
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18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Franco,G.R. and Pena,S.D.J., Unpublished Unpublished (1996)
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Strigeidida; Schistosomatoidea; Schistosomatidae; Schist
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SMEST]0390 Schistosoma mansoni, adult worm, Gloria Franco
Schistosoma mansoni cDNA clone SMPBE73 3' end, mRNA sequence
w06754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: (5531)4415611
Fax: (5531)4415409
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//lab host="XL1-Blue"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gfranco@mono.icb.ufmg.br
/note="Vector: BA vector; Site_1: NotI; Site_2: HindIII; Total cellular RNA from male and female adult worms was extracted according to a modification (Puissant, C. and Houdebine, L. M. BioFeedback 8, 148-149, 1990) of the Guanidine Thiocyanate procedure (Chomczynski, P. and Sacchi, N. Anal. BioChem. 162, 156-159, 1987). Poly (A)+RNA was purified by oligo dT column and cDNA was synthesized as described previously (Adams, M. D. et al. Nature Genet. 4, 373-389, 1993). cDNA was ligated to a
                                                                                                                                                                                                                                                                                                                                                                                Franco"
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Pred. No. 78;
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primer: M13 Forward.
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(5531)4415409
           /notes vector: BA vector; Site_1: NotI; Site_2: HindIII; /notes vector: BA vector; Site_1: NotI; Site_2: HindIII; /notes vector 
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electroporated into E. coli strain DH10B
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Seq primer: -28ml3 rev2 ET from Amersham
High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:619998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Washington University School of MedicineP
4444 Forest Park Parkway, Box 8501, St. Louis,
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 1 (bases 1 to 277)
Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T. Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA734164 277 bp mrNA linear EST 07-JAN-: vs19912.rl Barstead mouse irradiated colon MPLRB7 Mus musculus colone IMAGE:1138726 5' similar to gb:X80699 M.musculus L26 mRNA
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AA734164
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/note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; Tissue obtained from 8 week old mouse. Colon was harvested 72 hours after
                                                                                                                                                                                                                        /clone_lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         library was amplified and further selected for clones containing long inserts (>500 bp) by purification of the plasmid DNA from a fragment of a 1% low-melting-point agarose gel. containing the smear of the library and electroporation into DH10B cells. "

206 c 179 g 88 t 4 others
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/clone="IMAGE:1138726"
                                                                                                                                                                                                                                                                                                                                     /organism="Mus musculus"
/strain="FVB/N"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
Contact: Malcolm J. Gardner
Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 301 838 3519
Fax: 301 838 0208
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         Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutherla; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 624)
NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC)
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Gardner, M.J. and Kirkland, T.
Generation of ESTs from Coccidioides
                                                                                                                        BE896357.1
EST.
                                                                                                                                                    mRNA sequence
BE896357
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601439015F1 NIH_MGC_72 Homo
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/dev_stage-"spherule"
/lab_host-"SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Coccidioides immitis"
/db_xref="taxon:5501"
/clone="CIABC49"
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17; Conserv
                                                                                                                                                                                                        Contact: Blaxter ML
Institute of Cell, Animal and Pop
University of Edinburgh
Ashworth Labs, King's Buildings,
                                                                       Sequenced from the Brugia malayi BAC library constructed by Claire Whitton and Dr Mike Quail. The sequence was generated by The Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in collaboration with Mark Blaxter, ICAPB, University of Edinburgh, Edinburgh, UK.
                                                                                                                                                                                                                                                                                                    l (bases 1 to 631) Whitton,C., Daub,J., Ware,J., Quail,M., Hall,N., Barrell,B., Fosi,J., Guiliano,D., Slatko,B. and Blaxter,M. Genome survey sequences from the human parasitic nematode Brugia
                                                                                                                                                                                                                                                                                                                                                                        Brugia malayi
Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
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Tissue Procurement: ATCC/DCTD/DTP
                                            Seq primer: SP6
Class: BAC ends
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BH615799
                                                                                                                                                   Email: mark.blaxter@ed.ac.uk
                                                                                                                                                                                                                                                                        Unpublished (2000)
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/db_xref="taxon:9606"
/clone="IMAGE:3924266"
/organism="Brugia malayi"
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Barrell, B., Foster

GSS 28-JAN-2002

Edinburgh,

EH9

COMMENT DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM9761 row: m column: 03
High quality sequence start: 2
High quality sequence stop: 403.
Location/Qualifiers Contact: Robert Strausberg, Ph.D. cDNA Library Preparation: Life Technologies, cDNA Library Arrayed by: The I.M.A.G.E. Consc /clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pcMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
Technologies." Score 16.4; DB 10; Pred. No. 2.8e+02; 0; Mismatches 1; Consortium (LLNL) Length 624; 0; Gaps 0

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JOURNAL REFERENCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                            Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehlro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished 2 (bases 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fujlyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
Totoki,Y., Watanabe,H. and Sakaki,Y.
BAC end sequences of Library RPCI-43
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Pan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-001J13.TJ.
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17; Conserv
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
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R.Site 2
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/sex="Mixed (male and female)"
/tissue_type="whole parasite"
/dev_stage="microfilaria (L1)"
/note="Vector: pBACe3 6; Site_1: BamH I; Brugia malayi
genomic DNA was partially cleaved with Sau3A I and size
fractionated. 7,392 clones were generated with mean insert
size -48 kbp. The library was constructed by Claire
whitton, Blaxter Nematode Genetics Lab, University of
Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
Unit, The Sanger Centre, Cambridge, UK."
           ש
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"
299 c 145 g 252 t 10 others
                                                                                   /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-001J13.TJ"
                                                                        /sex≖"male"
                                                                                                                                                                                Location/Qualifiers
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/db_xref="taxon:6279"
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94.4%;
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Pred. No. 2.8e+02;
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Tel: 82-42-860-4473
Fax: 82-42-860-4479
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1 (bases 1 to 213)

Goh,S.-H., Park,J.-H., Lee,Y.J., Lee,H.G., Yoo,H.-S., Lee,I.-C., Park,J.-H., Kim,Y.-S. and Lee,C.-C.

Gene expression profile and identification of differentially expressed transcripts during human intrathymic T-cell development by cDNA sequencing analysis Genomics 70 (1), 1-18 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: gohsh@mail.kribb.re.kr
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KRIBB Human CD4 intrathymic T-cell cDNA library Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Thymus"
/cell_type="Intrathymic T-cell"
/dev_stage="CO3+4+8- single positive stage"
/note="Vector: pGEM-T; cDNA was made from total
cytoplasmic RNA of sorted human intrathymic CD3+4+8-
T-cell, adaptor ligated, amplified with PCR, and clor
into pGEM-T vector."
a 59 c 72 g 40 t 1 others
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/db_xref="taxon:9606"
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94.4%;
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Pred. No. 4.3e+02;
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Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers
, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk
, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann
public Soybean EST Project
Unpublished (1999)
Contact: Shopper
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available through: ResGen, Invitrogen Corp. 2130 South Memorial Parkway Huntsville, AL 35801 For further information call: (800)-533-4363 or contact via email: ccu@resgen.com
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
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90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Glycine max"
/db_xref="taxon:3847"
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/lab_host="XL10-Gold"
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Query Match Best Local Similarity

79.0%; 89.5%;

Score 15.8; DB 9; Pred. No. 5.3e+02;

Search completed: August 7, Job time: 22891 sec

2002, 21:15:21

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17;
                                                                                                                                                                                                                                                                                                  Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr
Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-FEB-2000) Genoscope - Centre BP 191 91006 EVRY cedex - FRANCE (E-mail: - Web: www.genoscope.cns.fr) 2 (bases 1 to 582)
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GSS.
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/note="end : SP6"
124 c 136 g 1
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/db_xref="taxon:7165"
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                                                                                    Length 582;
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Maximum DB seq length: 2000000000
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8: /SIDS1/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
        1736436 seqs, 858457221 residues
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Copyright (c) 1993 - 2000 Comp
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SUMMARIES

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	AAH51976	AAT09676	AAT29125	AAT29124	AAT29126	AAA49863	AAQ61457	AAA49826	AAA49824	ID
	Mycobacterium tube	Mycobacterium tube	rpoB gene fragment	rpoB gene fragment	rpoB gene fragment	Mycobacterium tube	M.tuberculosis rpo	Mycobacterium tube	Mycobacterium tube	Description

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ALIGNMENTS

RESULT AAA49824

AAA49824 standard; DNA; 20 ВP

AAA49824;

25-SEP-2000 (first entry)

Mycobacterium tuberculosis rpoB gene amplification primer rpoB-R.

Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;

Mycobacterium tuberculosis

WO200036142-A1.

22-JUN-2000.

10-DEC-1999; 99WO-CA01177.

11-DEC-1998; 98US-0111794.

(VISI-) VISIBLE GENETICS INC

Shipman R;

WPI; 2000-431611/37.

Method for the detection and characterization of Mycobacterium tuberculosis with antibiotic resistance in a sample - $\,$

Claim

4; Page 4; 43pp; English.

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CCCXX
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The present sequence is that of the
                             Claim 4; Page 5; 43pp; English.
                                                           Method for the detection and tuberculosis with antibiotic
                                                                                                             WPI; 2000-431611/37.
                                                                                                                                            Shipman R;
                                                                                                                                                                                                        11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-3s
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                                                                                                                                                                        (VISI-) VISIBLE
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                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the rpoB gene (see AAA49863). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and analysis of antiblotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                             characterization of Mycobacterium resistance in a sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amplification and cycle sequencing
Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 3
AAQ61457/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                 30-APR-1992;
14-AUG-1992;
16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                These primers can be used in a method for the detection and characterization of M. tuberculosis present in a sputum sample. The method involves performing a sequencing procedure, with or without prior amplification, to detect the presence of M. tuberculosis, and if present to evaluate the rpoB, katG, rpsL/sl2 and 23S genes for the presence of antibiotic inducing mutations. If M. tuberculosis is detected, a second sequencing procedure is performed on the sample to evaluate additional genes for the
                                                                                                             (INSP)
                         WPI; 1993-368812/46
                                                                                                                                                                                                                                                                                                             W09322454-A
                                                                                                                                                                                                                                                                                                                                          Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                      rifampicin; antibiotic; susceptibility; sensitive; resistant; rpoB;
mutant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                M.tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAQ61457 standard; DNA; 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpoB (rifampin resistance) gene sequencing primer rpoB-3s (bp 2611-2592). It is used with the forward primer given in AAA49825 and with the amplification primers given in AAA49823 and AAA49824 for the detection and analysis of antibiotic resistance-associated mutations of the rpoB gene (see AAA49863). Amplification and cycle sequencing
             P-PSDB; AAR51372
                                                                 Bodmer T,
                                                                                                                                                                                                                             17-SEP-1992;
                                                                                                                                                                                                                                                        30-APR-1993;
                                                                                                                                                                                                                                                                                    11-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                           17-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ61457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antibiotic treatment options.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      analysis of antibiotic resistance-associated mutations in define regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR (isoniazid), mabA (isoniazid), rpsL/sl2 (streptomycin), 165/rrs (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis. These primers can be used in a method for the detection and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the rpoB gene (see AAA49863). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and
                                                     Young
                                                                                                                                                      (ASSI-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          presence of antibiotic resistance-inducing mutations. Genotypersence of antibiotic resistance-inducing mutations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Conservative
                                                                                                                         ASSISTANCE PUBLIQUE INST PASTEUR.
MEDICAL RES COUNCIL
                                                                                              UNIV CURIE PARIS VI P & M.
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                                                  Cole S, Zhang Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP; 4
                                                                                                             BERNE.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                          tuberculosis
                                                                                                                                                                              92US-0875940.
92US-0929206.
93FR-0004545.
                                                                                                                                                                                                                                                                                                                                                                                                                rpoB
                                                                                                                                                                                                                           92FR-0011098
                                                                                                                                                                                                                                                        93WO-EP01063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Α;
                                                                 Heym
                                                                                                                                                                                                                                                                                                                                                                                                               gene fragment.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                 Honore N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 20; DB 2
Pred. No. 0.32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T; 0
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                                                                   Telenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in defined
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                rpsL/s12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
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RESULT 4
AAA49863/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local
The present sequence is that of the Mycobacterium tuberculosis rpoB (rifampin resistance) gene (bp2161-2640). Amplification cycle sequencing primers (see AAA49823-62) are used for the de and analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aph (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/rr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCR amplification was used to obtain rpoB genes from rifampicin-resistant Mycobacterium leprae strains. A comparison with the sequence of the rpoB gene from sensitive strains (AAQ51532) revealed mutations in the region encoding amino acids 400-450. The corresp. region was isolated from M.tuberculosis (AAQ61457). A common mutation seen in resistant strains occurs at codon 425 where Ser is substituted, most frequently by Leu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rapid detection of ant isoniazid, rifampicin by detecting mutation
                                                                                                                                                                                     Disclosure;
                                                                                                                                                                                                                                 Method for the detection and characterization of \mbox{\sc Mycobacterium} tuberculosis with antiblotic resistance in a sample -
                                                                                                                                                                                                                                                                                                                                                                Shipman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-JUN-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200036142-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    primer_bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Antibiotic resistance; rpoB gene; rifampin resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA49863 standard; DNA; 480 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 432 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                  (VISI-) VISIBLE GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 428
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                                                                                                                                                                                                                                                                                                               2000-431611/37
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|||||||||||||||||||||
TACGGCGTTTCGATGAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig
                                                                                                                                                                                     Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis rpoB gene (rifampin resistance)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0111794.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-CA01177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note "primer of the stage of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(41..60)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                     5; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78 A; 139 C; 148 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      antibiotic resistance in Mycobacteria -
cin or streptomycin resistance in tubercu
ion in katG, rpoB or rpsL genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of AAA49824"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of AAA49823"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  teria - esp.
tuberculosis
            oxyR-aphC
), 16S/rrs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                   detection
                                    PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 5
AAT29126/c
ID AAT29126 standard; DNA; 620
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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             characterization of M. tuberculosis present in a sputum sample. The method involves performing a sequencing procedure, with or without prior amplification, to detect the presence of M. tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s1: and 23S genes for the presence of antibiotic-inducing mutations. If M. tuberculosis is detected, a second sequencing procedure is performed on the sample to evaluate additional genes for the
                           Cleavage of nucleic acids using an enzyme, especially a nuclea selected from the group consisting of Cleavase (RTM) BN enzyme Thermus aquaticus DNA polymerase, Thermus thermophilus DNA polymerase, Escherichia coli ExoIII and the Saccharomyces cere Rad1/Rad10 complex. The nucleic acid substrate is preferably
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rpoB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis. These primers can be used in a method for the detection and
                 oligonucleotide containing a
                                                                                                                                             Cleavage of nucleic acids to detect mutation(s) - esp. in human p53 gene, to identify strains of mic
                                                                                                                                                                                      WPI;
                                                                                                                                                                                                                            Brow MAD,
                                                                                                                                                                                                                                                                              09-MAR-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                        30-AUG-1995;
09-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                               WO9615267-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                p53; mutant; mutation; cleavage; nuclease;
Escherichia; Saccharomyces; Campylobacter;
Staphylococcus; identification; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tests are rapid, sensitive and accurate providing information as antibiotic treatment options.
                                                                                                          Example 33;
                                                                                                                                                                                                                                                    (THIR-) THIRD WAVE TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                             09-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                       23-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT29126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  presence of antibiotic resistance-inducing mutations.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tacggcgtttcgatgaaccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene fragment (mutant) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACGGCGTTTCGATGAACCC
                                                                                                                                                                                      1996-259862/26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conserve 20;
                                                                                                                                                                                                              МĊ,
                                                                                                                                                                                                                           Dahlberg
                                                                                                         Page 306; 433pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 89 A; 153 C;
                                                                                                                                                                                                              Olive
                                                                                                                                                                                                                                                                             95US-0520946.
94US-0337164.
95US-0402601.
95US-0484956.
    microbial gene
                                                                                                                                                                                                                                                                                                                                             95WO-US14673
                                                                                                                                                                                                              JΕ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
                                                                                                                                                                                                                            Fors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 432
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ΒP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
human p53 gene sequence or e sequences. Cleavage products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 G;
                                                                                                                                                                                                                           ۲,
                                                                                                                                                                                                                                                      INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis
                                                                                                                                                                                                                            Heisler LM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cleavase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                             microorganisms
                                                                                                                                                                                                                           Lyamichev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
                                                                                                                                             allows detection croorganisms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genotypic
                                                                               nuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      rpsL/s12
                                           cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shigella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT 6
AAT29124/c
ID AAT291
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Best Loc
Matches
                                                                                                                                                                                                                                           30-AUG-1995;
09-NOV-1994;
09-MAR-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        compared to the cleavage products of reference gene sequences. The method is used for detecting mutation in the human p53 gene; for identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The method may also be used for the identification of viruses, especially hepatitis C virus (HCV) and similar immunodeficiency virus (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bg region of the Mycobacterium tuberculosis rpb gene, which, when mutated is associated with rifampin resistance. The 620 bp region amplified spans both the H451Y and S456L mutations. The amplified mutatic are given in AAT29124 (Wild type) and AAT29125-26
             oligonucleotide
                      Rad1/Rad10 complex.
                                                                                           Example
                                                                                                                                                              WPI; 1996-259862/26
                                                                                                                                                                                    Oldenburg
                                                                                                                                                                                                                                                                                                    09-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                          p53; mutant;
Escherichia;
                                                                                                                                                                                                                       (THIR-) THIRD
                                                                                                                                                                                                                                                                                                                           23-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                         Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                              Staphylococcus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAT29124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             μ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match
                                                                                                                                                                                                 MAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tacggcgtttcgatgaaccc
                                                                                                                                                                                                                                                                                                                                                                                                                                         gene fragment from Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TACGGCGTTTCGATGAACCC
                  e of nucleic acids using an enzyme, especially a nuclease id from the group consisting of Cleavase (RTM) BN enzyme, aquaticus DNA polymerase, Thermus thermophilus DNA ase, Escherichia coli ExoIII and the Saccharomyces cerevis idio complex. The nucleic acid substrate is preferably an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
20; Conserv
                                                                                           33;
                                                                                                                            human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences).
                                                                                                                                         0f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           620
                                                                                                                                                                                     č,
                                                                                                                                                                                    Dahlberg
MC, Olive
                                                                                                                           nucleic aci
an p53 gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.
ilarity 100.
Conservative
                                                                                           Page
                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces;
                                                                                                                                                                                                                                                                                                                                                                                                                   mutation; cleavage; nuclease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP;
                                                                                                                                                                                                                      WAVE TECHNOLOGIES
                                                                                                                                                                                                                                           95US-0520946.
94US-0337164.
95US-0402601.
95US-0484956.
                                                                                                                                                                                                                                                                                                                                                                         tuberculosis
  microbial
                                                                                                                                                                                                                                                                                                    95WO-US14673
       containing a human p53 gene sequence or
                                                                                                                                                                                                                                                                                                                                                                                              identification;
                                                                                         305; 433pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                            acids tene, to
                                                                                                                                                                                    DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201
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                                                                                                                           to detect of identify
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                          Campylobacter;
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                                                                                          English.
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                                                                                                                                                                                               Ļ
sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214
                                                                                                                                                                                                                       INC.
                                                                                                                                                                                                                                                                                                                                                                                              detection;
                                                                                                                                                                                                Heisler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G;
                                                                                                                          mutation(s) - allows detec
strains of microorganisms
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DВ
                                                                                                                                                                                               ĽM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Η,
Cleavage
                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                   cleavase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17;
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                                                                                                                                                                                               Lyamichev VI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 620
                                                                                                                                      allows detection
products
                                                                                                                                                                                                                                                                                                                                                                                                                 Thermus;
                                 cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                         Shigella;
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                                                                                                                           and
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Cleavage selected

Example

Page

305-306;

433pp;

English.

Thermus

Radi/Radio complex. The nucleic acid substrate is preferably oligonucleotide containing a human p53 gene sequence or alternatively, microbial gene sequences. Cleavage products as

Thermus aquaticus DNA polymerase, Thermus thermophilus DNA polymerase, Escherichia coli ExoIII and the Saccharomyces

e of nucleic acids using an enzyme, especially d from the group consisting of Cleavase (RTM) aquaticus DNA polymerase, Thermus thermophilu:

y a nuclease BN enzyme,

cerevisiae

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RESULT
AAT29125/
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esp. in h
                                                                                                                                                                                                                         30-AUG-1995;
09-NOV-1994;
09-MAR-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        method is used for detecting mutation in the human p53 gene; for identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter; Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The method may also be used for the identification of viruses, especially hepatitis C virus (HCV) and simian immunodeficiency virus (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bg region of the Mycobacterium tuberculosis robs gene, which, when mutated is associated with rifampin resistance. The 620 bp region amplified spans both the H451Y and S456L mutations. The amplified mutater region in AAT29124 (Wild type) and AAT29125-26 mutations are given in AAT29124 (Wild type) and AAT29125-26
                                                                                                                                                 WPI; 1996-259862/26
                                                                                                                                                                     Oldenburg
                                                                                                                                                                                                                                                                                                                                                                                                            rpoB
                                                                                                                                                                                                    (THIR-) THIRD
                                                                                                                                                                                                                                                                             09-NOV-1995;
                                                                                                                                                                                                                                                                                                    23-MAY-1996.
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                                                                                                                                                                                                                                                                                                                                              Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus;
                                                                                                                                                                                                                                                                                                                                                                            p53; mutant;
Escherichia;
                                                                                                                                                                                                                                                                                                                                                                                                                                 02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT29125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                compared to the cleavage products of reference gene sequences. method is used for detecting mutation in the human p53 gene; f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 620
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                 MAD,
                                                                                                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TACGGCGTTTCGATGAACCC
                                                                                                                  human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequences).
                                                                                                               of nucleic aci
human p53 gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; DNA; 620
                                                                                                                                                                    Dahlberg
MC, Olive
                                                                                                                                                                                                                                                                                                                                                                                                           fragment (mutant) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                            mutation; cleavage;
Saccharomyces; Campy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ВP;
                                                                                                                                                                                                    WAVE TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                              tuberculosis
                                                                                                                                                                                                                        95US-0520946.
94US-0337164.
95US-0402601.
95US-0484956.
                                                                                                                                                                                                                                                                               95WO-US14673
                                                                                                                                                                                                                                                                                                                                                                identification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              103
                                                                                                                c acids t
gene, to
                                                                                                                                                                    JE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
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                                                                                                                to detect
o identify
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
                                                                                                                                                                                                                                                                                                                                                                 Campylobacter;
ion; detection;
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                                                                                                                                                                                                    INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                     nuclease;
                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis
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                                                                                                             mutation(s) - allows detec
strains of microorganisms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20;
No.
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                                                                                                                                                                               ĽM,
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                                                                                                                                                                                                                                                                                                                                                                ; cleavase; Therm;
; Mycobacterium; ;
; ds.
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                                                                                                                                                                               Lyamichev VI,
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                                                                                                                         allows detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                           Shigella;
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Best Local S
Matches 20
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AAT09676 :
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 misc_feature
                                             misc_feature
                                                                                       misc_feature
                                                                                                                                   misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 620 BP; 103 A; 201 C;
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20; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 chain reaction;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                disease diagnosis; oligonucleotide; D
in reaction; DNA amplification; rpoB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tuberculosis rpoB
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433..434
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486
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438
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226 . 243
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226..240
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Pred.
                                                                                                                                                                                                                                                                                    rpo95"
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                                                                                                                                                                                                                                          rpo105'
                                                                                                                                                                                                                                                                                                                                   "HQIQG
                                                                                                                                                                                                                                                                                                                                                                               DDIDHL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene DNA sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 T; 0 other;
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0.38;
               signature
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B locus; TB;
               nucleotide'
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671
              1 tacggcgtttcgatgaaccc
TACGGCGTTTCGATGAACCC
                                                                        Similarity
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This oligonucleotide DNA primer is specific for Mycobacterium tuberculosis, and may be used to amplify a sample DNA by targeting a portion of the gene encoding rpoB. The 1st several bases comprise nonhybridizing tail consisting of filler bases followed by a restriction site incorporated to facilitate cloning using the amplicon at a later date, if desired. The remaining bases hybridize to bacterial rpoB DNA. The method provides for the detection of M. tuberculosis and the concurrent determination of its drug
                          susceptibility, particularly to rifamycin. The method can provide often greater than 95% sensitivity and 100% specificity. The biological sample is a fluid or tissue sample from a human.
                                                                                                                                                                                                                             Disclosure;
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 Sequence
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Young KKY;
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970 BP; 182 A;
                                                                                                                                                                                                                           Fig.3; 54pp;
                                                                                                                                                                                                                                                                                                                                                         Hunt JM,
                                                                                                                                                                                                                                                      Mycobacterium tuberculosis - by amplifying sample DNA set that targets portions of the gene encoding rpoB.
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952..966
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536..562
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primer
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 302 C;
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330 G;
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156 T; 0
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100.0%; ilarity 100.0%; Conservative

Score 20; [Pred. No. 0.

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17; 0.

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970; 0:

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Mismatches

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RESULT 10
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AAH51976/c
                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This invention relates to a method for identifying a nucleotide or polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polynucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of an organism
                                                                                                                                                                                                                               12-NOV-1999;
12-NOV-1999;
01-FEB-2000;
24-JUL-2001
                                                   AAH02079;
                                                                                                      AAH02079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure;
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DB; AAG81125.
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1 Similarity 100.0%;
20; Conservative 0
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                                                                                                   standard;
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99US-0165124.
2000US-0179531.
(first entry)
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The present invention describes a method for generating a repertory of CC nucleic acids of tuf, fus, atpD and/or recA genes from which probes CC and/or primers are derived: The method comprises amplifying the nucleic CC acids of determined algal, archaeal, bacterial, fungal and parasitical CC species with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more CC related microorganisms e.g. algae, archaea, bacteria, fungi and CC parasites, for universal detection and for specific and ubiquitous CC detection and identification of an algal, archaeal, bacterial, fungal and parasitical species, genus, family and group. A nucleic acid (I) CC obtained using the method of the invention can be used for the universal CC detection of any bacterium, fungus or parasite in a sample and for the CC detection of at least one antimicrobial agent resistance gene or at CC least one toxin gene. hexa nucleic acids are used for the specific and CC ubiquitous detection and for identification of Streptococcus pneumoniae. CC (I) can be used to design a therapeutic agent which is effective against CC microorganisms. Microbial species or genus or family or phylum or group CC which can be detected include Abiotrophia adiacens, Bordetella sp., CC wynebacteriaceae family, Pseudomonads group, Escherichia coli, CC Mycobacteriaceae family pseudomonads group, Escherichia coli, CC Mycobacteriaceae family pseudomonads group, Escherichia coli, CC Mycobacteriaceae
                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic acid sequences are used to generate universal probes primers which can be used to identify and detect the presence archaeal, bacterial, fungal and parasitical species in a test
                                                                                                               Sequence
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19-MAY-2000; 2000CA-2307010
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100.0%; llarity 100.0%; Conservative 0;
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                                                                                                               ВP;
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                                                                                                             679 A; 1081 C;
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Score 20; DI
Pred. No. 0.4
); Mismatches
                                                                                                             1188 G;
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                                         DB 22;
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e presence of algal,
in a test sample -
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XID AAA746
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XID AAA746
XID AAA746
XID AAAA746
XID AAA746
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X O X K X X D X D X A 
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 12
AAA89994/c
ID AAA89994 standard;
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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is the rpoB gene from Mycobacterium tuberculosis. Rifampin resistance is largely associated with point mutations localised in a small core region of 81 base pairs in the rpoB gene, which encodes the RNA polymerase beta subunit. To detect a mutation, a complex is formed comprising a first sequence representing the predetermined region of the gene of the organism and a second sequence representing the corresponding region of the gene of the wild type organism in double stranded form. Each member of at least one pair of non-complementary strands within the complex has a label. The association of the labels in the complex is related to the presence of the mutation. The presence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2122
                               Mycobacterium tuberculosis
                                                                                                                                                                                                                  M. tuberculosis
                                                                                                                                                                                                                                                                                           18-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                 AAA89994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200043546-A2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA74651;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA74651 standard;
                                                                                                     RNA polymerase beta subunit;
                                                                                                                                    Drug resistance; rifampin; rifampicin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method for detecting drug resistance in a strain of an organism, particularly for detecting rifampin resistance in Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Liu YP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DADE-) DADE BEHRING INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 tacggcgtttcgatgaaccc 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TACGGCGTTTCGATGAACCC 2103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3853
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F1g
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                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     вP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tuberculosis rpoB gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   related
                                                                                                                                                                                                              rpoB gene encoding RNA polymerase beta subunit.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 723 A; 1173 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to the drug
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                                                                                                                                                                                                                                                                                                                                                                                                                                       ВP
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                                                                                                         d9
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1293 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20;
                                                                                                                                    pyrazinamide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .42;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     other;
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RESULT 1
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Best Local
                                                                                                                                                            primer; dif
rifabutin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This invention relates to a method for detecting drug resistance in a strain of an organism. The method comprises detecting the presence of a least 1 mutation in a first sequence and relating the presence of the mutation to drug resistance. Included in the invention are a kit for carrying out the method and a method for detecting the presence of a difference between two related nucleic acid sequences in an organism. I methods are useful for detecting resistance to drugs such rifampin and pyrazinamide in Mycobacterium. The present sequence represents the Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase beta subunit). The sequence is used in an example of the method of the invention for the detection of rifampin resistance in M. tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting resistance of drugs such as rifampicin Mycobacterium, comprising detecting mutations in them to drug resistance -
                                                                                                                                       Synthetic.
                                                                                                                                                                                                                       M. tuberculosis rpoB gene fragment amplification primer
                                                                                                                                                                                                                                                                     AAT12096;
                                                                                                                                                                                                                                                                                             AAT12096 standard;
                                                                                                                                                                                                                                                                                                                                                      2122 TACGGCGTTTCGATGAACCC 2103
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3853 BP; 723 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-JAN-1999;
22-APR-1999;
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                    (INNO-) INNOGENETICS NV
                                             09-JUN-1994;
                                                                  09-JUN-1995;
                                                                                          14-DEC-1995
                                                                                                                 W09533851-A2
                                                                                                                                                                                    determination;
                                                                                                                                                                                                Antibiotic;
                                                                                                                                                                                                                                              10-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 1; Fig
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                                                                                                                                                                         differential;
                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                            species
                                                                                                                                                                                               resistance; spectrum; gene; mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                    amplification;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4; 91pp;
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99US-0296894
                                            94EP-0870093
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                                                                   95WO-EP02230
                                                                                                                                                                                                                                                                                             DNA;
                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                        hybridisation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              1173 C; 1293 G;
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                                                                                                                                                                                                                                                                                             ВP
                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                               Score 20;
Pred. No.
                                                                                                                                                                                    tuberculosis; rpoB;
                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                        pattern; rifampicin;
                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                             ВB
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                                                                                                                                                                                                                                                                                                                                                                                                               .42;
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a gene and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              other;
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relating
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De Beenhouwer H,

Jannes G,

Machtelinckx L,

Portaels

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RESULT 14
AAQ51532/c
  PAARRA PRARRA PAARARA 
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Best Local S
Matches 19
                                                                                                                                              17-SEP-1992;
30-APR-1992;
14-AUG-1992;
16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The antibiotic resistance spectrum (ARS) of a mycobacterium can be determined by amplifying the relevant part of the antibiotic resistance gene, i.e. the M. tuberculosis rpoB gene fragment amplified using the primer set AAT12091-98, hybridising it with a least 1 rpoB gene probe, detecting the hybrids formed and inferring the ARS, and opt. the spp., from the differential hybridisation patterns. The method spartic. useful for the detection of rifampicin and/or rifabutin resistance in M. leprae or M. tuberculosis, and mycobacterial spp. identification. The method is rapid and reliable and provides simultaneous determn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M.leprae
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Mycobacterium, opt. coupled with species identification - from
different patterns of hybridisation with rpoB gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rifampicin; mutant; ss.
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                      (ASSI-)
(INSP)
(MEDI-)
(UYBE-)
                                                                                                                                                                                                                                                                                                                      11-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium
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92US-0875940.
92US-0929206.
93FR-0004545.
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Best Local
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                                                                                                                 21-MAR-2000;
23-MAY-2000;
26-MAY-2000;
23-OCT-2000;
23-OCT-2000;
27-NOV-2000;
16-FEB-2001;
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DB; AAR43671.
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DB; AAU33498.
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CC Note: The sequence data for this patent did not form part CC format directly from WIPO at CC format directly from WIP
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Best Local Similarity 90.0
Matches 18; Conservative
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ALIGNMENTS

KEYWORDS SOURCE ORGANISM ACCESSION VERSION FEATURES RESULT 1 MSGRIFRNAP/c REFERENCE DEFINITION TITLE AUTHORS JOURNAL source RNA polymerase beta-subunit; rifampicin resistance.
Mycobacterium tuberculosis (strain H37) DNA.
Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
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/protein_id="AAB59068.1"
/db_xref="GI:149992"
/tanslation="GMRTLRTVGELIONQIRVGMSRMERVVRERMTTQDVEAITPQTL
INIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDV
INIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDV
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1 (bases, M.W., Lyamichev, V.I. and Lyamichev, N.

Cleavage of nucleic acid acid using thermostable methoanococcus
                                                  Unknown
                                                                                            Sequence 136 from patent AR062057
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Patent: US 5843669-A 135 01-DEC-1998;
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Sequence 135 from
AR062056
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AR067448.1 GI:5998670
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Patent: US 5851763-A 59 22-DEC-1998;
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Sequence 138 from patent
AR062059
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Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.

Clearvage of nucleic acid acid using thermostable methoanococcus

jannaschii FEN-1 endonucleases

Patent: US 5843669-A 138 01-DEC-1998;
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Patent: US 5843669-A 136 01-DEC-1998;
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                                                                                                                                                                                                                                                                                   AR062061 620
Sequence 140 from patent US
AR062061
AR062061.1 GI:5989752
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Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.
Cleavage of nucleic acid acid using thermostable methoanococcus
Jannaschii FEN-1 endonucleases
Patent: US 5843669-A 139 01-DEC-1998;
Location/Qualifiers
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                                                                                                  Score 20; DB Pred. No. 1.4;
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DEFINITION

AF060353 Mycobacterium

tuberculosis RNA polymerase beta-subunit (rpoB) gene,

linear

BCT 15-MAY-1998

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REFERENCE
AUTHORS
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ACCESSION
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AR149128/c
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VERSION
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JOURNAL
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Best Local
               JOURNAL
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                                                                                                                                                                                Sequence 24
AR149128
AR149128.1
                                          Unclassified.

1 (bases 1 to 706)
Gingeras, T.R., Mack, D., Chee, M.S., Ber Ghandour, G. and Wang, C.
Chip-based species identification and
                                                                                                                                  Unknown
                                                                                                                                                                                                                                    AR149128
                                                                                                                                                                                                                                                                                                                                                                                        20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gingeras, T.R., Ghandour, G., Drobniewski, F., Alland, D., I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Genome Res. 8 (5), 435-448 (1998) 98248685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gingeras,T.R., Ghandour,G., Wang,E., Berno,A., Small,P.M., Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Drenkow,J. Simultaneous genotyping and species identification using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis
Bacteria; Filmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
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AF060353
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                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ibmitted (20-APR-1998) Division of Infectious Disease, Affymetrix,
380 Central Expressway, Santa Clara, CA 95051, USA
            microorganisms
tent: US 6228575-A 24 08-MAY-2001;
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                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
llarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="QDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT HKRRLSALGFGGLSRERAGLEVADVHFSHYGRWCPIETPEGPHIGLIGSLSVYARVNP FGFIETPYRVVDGVVSDEIVYLTADEDRHVVAQANSPIDADGRFVEPRVLVRRKAG EVEYVPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMQRQAVPLVRSEAP LVGTGMELRAAIDAT"
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
/product="RNA polymerase beta-subunit"
/protein_id="AAC38533.1"
/db_xref="GI:3133465"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /strain="ATCC27294"
/db_xref="ATCC:27294"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              organism="Mycobacterium tuberculosis"
                                                                                                                                                                                  GI:15113719
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Pred. No. 1
                                                                            Chee, M.S., Berno, A.J., Stryer, L.,
                                                                                                                                                                                                                                      706 bp
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Desmond, E.,
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                                            phenotypic characterization
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AX111339/c
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BASE COUNT
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AX111339
                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                   Highly conserved genes and their use to for detection of microorganisms Patent: WO 0123604-A 2072 05-APR-2001; Infectio Diagnostic (I.D.I.) INC. (CA) Location/Qualifiers
                                                                                                                                                                                         Mycobacterium tuberculosis.
Mycobacterium tuberculosis
Mycobacteria; Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 3534)

Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M., Picard, F.J. and Roy, P.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 970)
Persing, D.H., Hunt, J.J., Young, K.K.Y., Felmlee, T. and Whelan, A.Christian.
Detection of a genetic locus encoding resistance mycobacterial cultures and in clinical specimens Patent: US 5643723-A 1 01-JUL-1997;
                                                                                                                                                                                                                                               AX111339.1
                                                                                                                                                                                  Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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20; Conser
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2072 from Patent W00123604.
                                                            1. .3534
                                 /organism="Mycobacterium tuberculosis"
/strain="Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GI:2472409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism∞"unknown"
302 c 330 g
                       /db_xref="taxon:1773"
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227 c 250 g
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           1081 c
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       1188 g
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Pred. No.
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s 5643723.
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                                                                                                                    generate probes and primers
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                                                                                                                                                                                                                                                                                  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteridaee;
Actinomycetales; Corynebacterineae; Mycobacteridaeeae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (11-JUL-1994) Paul Imboden, Institute for Medical Microbiology, University of Berne, Friedbuehlstrasse 51, Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cole,S., Schopfer,K. and Burkart,T.
The rpoB gene of Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB) gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Imboden, P., Troller, R., Marchesi, F., Telenti, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 1851)
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                                                                                                                                                        HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRMCPIETPEGPNIGLIGSLSVYARVNP
FGFIETPYRKVVDGVVSDGIYYLTADBEDRHYVAQANSPIDADGREVEPRVLVRRKAG
EVEYVPSSEVDYMDVSPRQMVSVATAMLFFLEHDDANRALMGAMMQRQAVPLVRSEAP
LVGTGMELRAAIDAATSSQESGVIEEVSADY ITVMHDMGTRRTYRMRKFARSHNGTC
ANQCPIVDAGGRVEAGQVIADGPCTDDGEMALGKNLLVAIMPMEGHNYEDAIILSNRL
VEEDVLTSIHIEEHEIDARDTKLGABEEITRDIPNISDEVLADLDERGIVRIGAEVRDG
DILVGKVTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGESGKVIGIRVESRED
                                                                                        ILNTHGVPRRMNIGQILETHLGWCAHSGWKVDAAKGVPDWAARLPDELLLEAQPNAIVS
TPVFDGAQEAELQGLLSCTLPNRDGDVLVDADGKAMLFDGRSGEPFPYPVTVGYMYIM
                                                                                                                                                                                                                                                                                                                             RDYGURIDAKRROPUTVLIKALGWYSEQIVERFGFSEIMRSTLEKDMYVGTDEALLD
IYRKLRPGEPPTKESAOTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
EEDVVATIELVRLHEGOTTWIVPGGVEVPVETDDIDHFGNRILRTVGEILJQNOIRVG
MSRMERVVRERMTTODVEAITPOTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
                                                                                                                                                                                                                                                                                                                                                                                                                           REPLEVPGLLDVQTDSFEWLIGSPRWRESAAERGDVNPVGGLEEVLYELSPIEDFSGS
MSLSFSDPRFDDVKAPVDECKDKDMTYAAPLFVTAEFINNNTGEIKSQTVFMGDFPMM
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/db_xref="GI:7144499"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="H37Rv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MLEGCILADSROSKTAASPSPSRPOSSSNNSVPGAPNRVSFAKL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene-"rpoB"
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                   1293 g
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MSGRPOB/c
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Miller, L.P., Crawford, J.T. and Shinnick, T.M. Miller, L.P., Crawford, J.T. and Shinnick, T.M. The rpoB gene of Mycobacterium tuberculosis antimicrob. Agents Chemother. 38 (4), 805-81.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            L27989.1 GI:468333
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                                                                                                                                                                                                                                                                                                                                                    MSLSFSDPRFDDVKAPVDECKOKDMYYAAPLFVTAEFINNNTGEIKSQTVFMGDFPMM
TEKCTFIINCTERVVVSQLVRSPGVYFDETIDKSTDKTLHSVKVIPSRGAMLEFDVDK
RDTVGVRIDKERGPVTVLLKALGWTSEGIVERGFFSEIMRSTLEKDNTVGTDEALLD
IYRKLRPGEPPTKESAGTLLEBLFFKERRYDLARVGRYKVNKKLGLHVGEPITSSTLT
EEDDVATIEKLNFRLHEGOTTMTVPGGVEVPVETDDIDHFGNRRLETVGELLONQLRVG
MSRMERVVRERMTTQDVEAITPQTLINIFPVAAIKEFFGTSQLSQFMDQNNPLSGLT
HKRLSALGPGGLSKEREAGLEVVDDVHPSHYGRMCPIETPEGPNIGLIGSLSVYARVNP
FGFIETPYRKVVDGVVSDEIVVLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG
EVEYVPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANGALMANGRQAVPLVRSEAP
LVGTCMELLRALDAATSSSQESGVIEEVSADYITVMHDNGTRRTYRMKKEARSNHCTC
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VEEDVLTSIHIEEHEIDARDTKLGAESIKADEVLADLDERGIVGIAVEGRED
DILVGKVTPKGETELFPEERLLRAIFGBKRAGKGVIGKVFGRED
DILVGKVTPKGETELFPEERLLRAIFGGKAREVADTSLKVPHGESGKVIGIRVEGSRED
DILVGKVTPKGETELFPEERLLRAIFGGKAREVADTSLKVPHGESGKVIGIRVEGSRED
DEDELPAGVNELVRVYAQKRKISDGDKLAGRHONKGVIGKILVEDDMFFLADGTFYDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="rpoB"
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/gene="rpoB"
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4641. .>5084
                                                                                                                                                                                                                                                        KLHHLVDDKIHARSTGPYSMITQQPLGGKAQFGGORFGEMECWAMQAYGAAYTLQELL
TIKSDDTVGRVKVYEAIVKGENIPEPGIPESFKVLLKELQSLCLNVEVLSSDGAAIEL
                                                                                                                                                                                                                                                                                                          TPVFDGAQEAELQGLLSCTLPNRDGDVLVDADGKAMLFDGRSGEPFPYPVTVGYMYIM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /evidence-experimental
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/protein_id="AAA21416.1"
/db_xref="GI:468334"
                                                                                                                                                                                                                                   REGEDEDLERAAANLGINLSRNESASFEDLA"
                                                                                                                                                                                                                                                                                                                                    TLNTHGVPRRMNIGQILETHLGWCAHSGWKVDAAKGVPDWAARLPDELLEAHANAIVS
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/transl_table=11
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1065. .4598
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/strain="Rv"
                                                                                                                              /gene="rpoC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MLEGCILADSRQSKTAASPSPSRPQSSSNNSVPGAPNRVSFAKL"/
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Pred. No. 2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
Submitted (25-APR-2001) The Institute for the subm
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fleischmann,R.D., Alland,D., Eisen,J.A., Carpenter,L., White,O. Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E., Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ermolaeva,M., Salzberg,S.L., Delcher,A., Utterback,T., Weidman,J., Khouri,H., Sill, J., Mikula,A. and Bishai,W.
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1 (bases 1 to 19352)
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GLFCEKLFGPTROWECYCGKYKRYRFKGIICERCGVEVTRAKVRRERMGHIELAAPVT
HIWYFKCVPSRLGYLLDLAPKDLEKIYFAAYVITSVDEEMRHNEL"
a 1534 c 1691 g 890 t
REPLEVPGLLDVOTDSFEWLIGSPRKRESAAERGDVUKPVGGLEEVLYELSPIEDFSGS
MSLSFSDRFDDVKAPVDECKNEDMT AF AFTEV
MSLSFSDRFDDVKAPVDECKNEDMT AF AFTEV
MSLSFSDRFDDVKAPVDECKNEDMT AF AFTEV
MSLSFSDRFDDVKAPVDECKNEDMT AF AFTEV
MSLSFSDRFDVGKTLHSVEVIPSRGVEV
MSLSFSDRFLDKTLHSVEVIPSRGVEV
REDTVGVRIDRKRROPVTVLLKALGWTSEQIVERFGFSEIMRSTLEKDNTVGTDEALLD
IYRKLRPGEPPTKESAQTLLENLFFKERTDLAPKTKVNKKLGLHVGEPITSSTLT
EEDVVATIELVRLHEGGVEVPVETDDLDHFGNRRLRTVGETLINKOITVG
MSRMERVVRERMTTQDVEAITPOTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene=1
                                                                                                                                                                                                                                                                                                                                                                                      /product="DNA-directed RNA polymerase, beta subunit"
/protein_id="AAK44921."
/db_xref="Gi:13880218"
/translation="MLEGCILADSROSKTAASPSPSRPOSSSNNSVPGAPNRVSFAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="similar to GB:L27989 PID:149992; identified by se
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/strain="CDC1551"
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l63. .3699
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FGF1ETPYRKVVDGVVSDEIVYLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG EVEYVPSSEVDYMDVSPRQMVSVATAMIFFLEHDDANIRALMGAMMQRQAVFLVRSEAP LVGTGMELRAAIDAGDVVVAEESGV1EEVSADYITVMHDNGTRRTYRMRKFARSNHGT CANQCQFIVDAGDRVEAGQVIADGPCTDDGEMALGKNLLVAIMPWEGHNYEDAIILSNR LVEEDVLTSIHIEEHEIDARDTKLGAEEITRDIPNISDEVLADLDERGIVRIGAEVRD GDILVGKVTPKGETELTPEERLLRAIFGEKAREVRDTSLKVPHGESGKVIGIRVFSRE DEDELPAGVNBLVRVVVAQKRKISDGDKLAGRHGNKGVIGKILVEVEDMPFLADGTPVD IILNTHGVPRRMIGGILEFHLGWCAHSGWKVDAAKGVPDMAARLPDELLEAQDHAIV STPVFDGAQEAELQGLLSCTLPNRDGDVLVDADGKAMLFDGRSGEPFPXPVTVGYMYI /gene="MT0696" 3744. .7694 3744. .7694 MKLHHLVDDKIHARSTGPYSMITQQPLGGKAQFGGQRFGEMECWAMQAYGAAYTLQEL LTIKSDDTVGRVKVYEAIVKGENIPEPGIPESFKVLLKELQSLCLNVEVLSSDGAAIE /note="similar to SP: similarity; putative" LREGEDEDLERAAANLGINLSRNESASVEDLA" /gene="MT0696" SP:P37871; identified by sequence

gene

CDS

/product="DNA-directed /transl_table=11 /codon_start=

d RNA

polymerase,

beta-prime subunit"

EDDINGTETICLA POLITION OF THE PROPERTY OF THE PVLMGITKASLATDSWLSAASFQETTRVLTDAAINCRSDKLNGLKENVIIGKLIPAGT GINRYRNIAVQPTEEARAAAYTIPSYEDQYYSPDFGAATGAAVPLDDYGYSDYR" GVCATCYGRSMATGKLVDIGEAVGIVAAQSIGEPGTQLTMRTFHQGGVGEDITGGLPR VQELFEARVPRGKAPIADVTGRVRLEDGERFYKITIVPDDGGEEVVYDKISKRQRLRV /translation="MLDVNFFDELRIGLATAEDIRQWSYGEVKKPETINYRTLKPEKD GLFCEKIFGPTRDWECYCGKYKRVRFKGIICERCGVEVTRAKVRRERMGHIELAAPVT complement(7691. VSIHDKHIEVIVRQMLRRVTIIDSGSTEFLPGSLIDRAEFEAENRRVVAEGGEPAAGF FKHEDGSERVLSDGDHVEVGQQLMEGSADPHEVLRVQGPREVQIHLVREVQEVYRAQG <u>AVEDQRDGELEARAQKLEADLAELEAEGAKADARRKVRDGGEREMRQTRDRAQRELDR</u> HIWYFKGVPSRLGYLLDLAPKDLEKIIYFAAYVITSVDEEMRHNELSTLEAEMAVERK /protein_id="AAK44922... /db_xref="GI:13880219"

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gene

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γď

CDS gene

+

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ALECLGGNGY VEDSGMPRLY REAPLMG I WEGSGNVSALDTLRAMATRPACVEVLFDEL
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                                                                                                                                                                                                                                                   14439
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                                  Query Match
Best Local Similarity
Matches 20; Conserv
1709 TACGGCGTTTCGATGAACCC
        1 tacggcgtttcgatgaaccc
                                   Conservative
                                           100.0%;
1690
                 20
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Search completed: August 7, 2002, 21:51:46 Job time: 23881 sec

gene CDS

Title: Perfect score:

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tacggtcggcgagctgatcc

Scoring table: Sequence:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Run

95:

August

7,

2002, 21:15:20 ;

OM nucleic -

nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

Database

EST:*
1: em,
2: em,
3: em
4: em
6: er
6: er
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9: 9:
110:
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114:
115:

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Minimum DB Maximum DB

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2000000000

Total number of Searched:

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University of Chicago
920 E. 58th Street, Chicago,
Tel: 773 702 4374
Fax: 773 702 3172
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Tetrahymena thermophila
Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM397871 130 bp mRNA linear EST 17-JAN-2002 5009-0-38-C10.t.1 Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence. BM397871.1 GI:18197924 EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2002)
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Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E.,
J. and Klobutcher, L.
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Proc. Natl. Acad. Sci USA, 98: 8709-8713."
a 41 c 44 g 18 t 1 others
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BM320964
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BE6263401
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   Score 18.4; DB 10;
Pred. No. 1.7e+02;
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                               Length 130;
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BH402082 AG-ND-156
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o	H	18.4	92.0	130	10	вм397871	вм397871 5009-0-38
ი	N	18.4	92.0	132	10	вм396091	
O	w	18.4	92.0	134	10	вм398255	BM398255 5009-0-42
ი	4	17.4	87.0	984	12	CNS01GJZ	AL143232 Anopheles
	Ç	17	85.0	422	10	BE443802	BE443802 WHE1122_I
	σ	17	85.0	544	10	BE445100	BE445100 WHE1132_I
	7	17	85.0	558	10	BE444713	BE444713 WHE1137_F
	00	17	85.0	610	ø	BE195103	BE195103 HVSMEh008
	9	17	85.0	658	10	BE442518	BE442518 WHE1101_F
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O	11	16.8	84.0	419	10	BI188703	BI188703 d2e05fs.:
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Ω	13	16.8	84.0	640	10	BI888442	BI888442 ZF637-2-(
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Ω	16	16.4	82.0	402	ဖ	BE101908	BE101908 UI-R-BO1-
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SOURCE
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Contact: Turkewitz AP Molecular Genetics and
                                          EST from Tetrahymena thermophila, strain Unpublished (2002)
                                                                                            Turkewitz,A.P., Karrer,K.M., Jahn,C.,
,J. and Klobutcher,L.
                                                                                                                                                            Tetrahymena thermophila.
Tetrahymena thermophila.
Tetrahymena thermophila.
Eukaryota, Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
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Tel: 773 702 4374
Fax: 773 702 3172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells
Unpublished (2002)
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
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920 E. 58th Street, Chicago,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular Genetics and Cell Biology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Turkewitz, A.P., Karrer, K.M., Jahn, C., Orias, E., Kirk, K.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hymenostomatida; Tetrahymenina;
1 (bases 1 to 132)
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                                                                                                                                    (bases 1 to 134)
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/strain="CG428.1"
/db_xref="taxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
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/clone_lib="Chilcoat"/
/clone_li
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95.0%;
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CNS01GJZ 984 bp DNA linear GSS 01-JUN-2001 Anopheles gambiae GSS T7 end of clone 06016 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                         Submitted (16-FEB-2000) BBMI, Institut Pasteur, 25, rue du Dr Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Blochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.
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920 E. 58th Street, Chicago,
Tel: 773 702 4374
Fax: 773 702 3172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 (bases 1 to 984)
Roth, C.W., Brey, P.T., Ke, Z.,
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                                                                                                                                    /db_xref="taxon:7165"
/clone="06016"
/clone_lib="NotreDame1"
/note="end: T7"
a 236 c 241 g 23:
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/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."

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/strain="PEST"
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/strain="CU428.1"
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Malloreae; Normalized root cDNA library

Mopublished (2000)

Contact: Olin Anderson

US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center

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Tel: $105595818
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Location/Qualifiers
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                                                                                                           Similarity
                                                                                                                                                                                                                                                 84
                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                  /notes "vector: Lambda Uni-ZAP XR, excised phagemid phluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxine in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of
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                                                                                                                                                                                                                                        preparations and DNA sequencing were preparations and UNA sequencing were Anderson lab (all other authors)."

130 c 124 g 84 t
                                                                                                                                                                                                                                                                                                                     normalization was carried out. The mass excision of phagemid library and normalization were done in HT Ng lab by D. Zhang at Texas Tech Univeristy. Normalization of the control used was that of Soares. Plasmid DNA
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/db_xref="taxon:4565"
/cloxe="WHE1122_B06_C12"
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/lab_host="E. coli DH10B"
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                                                                               Score 17; DB; Pred. No. 9.2 0; Mismatches
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BE445100
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US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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1 (bases 1 to 544)

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han ,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library
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/cultivar="Chinese Spring"
/db_xref="taxon:4565"
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/lab_host="E. coli DH10B"
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1 (bases 1 to 558)

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han p.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Passch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D. The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library
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West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
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                                                                                                                                                                                                                                              nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech University. Normalization preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host="E. coli DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid pBluescript SK, Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1137_H03_005"
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                                                                                                  85.0%; Score 17; DB
100.0%; Pred. NO. 9.1
:ive 0; Mismatches
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9.8e+02;
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RESULT

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Query Match Matches

Local Similarity hes 17; Conserv

Conservative

85.0%; Score 17; DB 100.0%; Pred. No. le-tive 0; Mismatches

1e+03;

Length 610; Indels

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HVSMEh0088E21f Hordeum vulgare 5-45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0088E21f,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Close,S.J., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource
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BE195103.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 On Jun 26,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         primer: AATTAACCCTCACTAAAGGG
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864 656 4293
                               127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rwing@clemson.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wing RA
                                                                                                                                                                                                                                                                                                                                                         Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Hordeum vulgare 5-45 DAP spike EST library HVcDNA0009 (5 to 45 DAP)"
                         http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" 203 c 158 g 120 t 2 others
                                                                                                                                                                                                                                                                                                 The sequence has been trimmed to remove vector sequence and contains a minimum of 100\ \mathrm{bases} of phred value 20\ \mathrm{o}
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/cultivar="Morex"
                                                                                                                                                                                                                                        sequence analysis see
                                                                                                                                                                                                                                                                           above, For more details on library preparation and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:4513"
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4 ggtcggcgagctgatcc 20
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Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T.,
Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat
genomes - Normalized root cDNA library
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence have been
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uence have been trimmed to remove vector sequence and
lity sequence with phred score less than 20
primer: Stratagene SK primer.
location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
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/cultivar="Chinese Spring"
/db_kref="taxon:4565"
/clone="WHE1101_H10_019"
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/lab_host="E. coli DH10B"
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1 (bases 1 to 828)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.V., Fenton,R.D. and Main,D.
Development of a genetically and physically anchored EST resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BG299722 828 bp mRNA linear EST 17-OCT-2001
HVSMEa0021120f Hordeum vulgare seedling shoot EST library
HVcDNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0021120f,
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100 Jordan Hall, C
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                                                                                                                                                                                                                                                                                                                                                       phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main ). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 5oC for 2 days. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 600000 pfu were in vivo excised to give pBluescript SK() cDNA the contraction of the contracti
this clone see http://www.genome.clemson.edu/orders A. see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST rescures for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html) (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html) 271 c 220 g 165 t
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HVcDNA0001 (Cold stress)"
                                                                                                                                                                                                                                                                          sequence analysis see
http://www.genome.clemson.edu/projects/barley.
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/lab_host="TJC121"
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RESULT 12
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similar to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 73 2.2 gi|7799258|emb|CAB90 (AL355752) putative integral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             620 Parrington Oval, Norman, Tel: 405 325 4912
Fax: 405 325 7762
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Other_ESTs: d2e05fs.f1
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Analysis of a Fusarium sporotrichioides EST database
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Location/Qualifiers
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cDNA library"
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/clone="d2e05fs"
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/strain="Tri 10"
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606 bp mRNA linear EST 24-OCT-2001 adult brain Danio rerio cDNA clone 5333151 5' Q9Y4D4 KIAA0648 PROTEIN ;, mRNA sequence.
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MPMGp637 Danio
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Fax: 314 286 1810
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Unpublished (1998)
Other_ESTs: fu53f08.x1
Contact: Stephen L. Johnson
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. 1
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Matthew Clark. DNA Sequencing by: Washington University Genome
Matthew Clark DNA Sequencing by: Washington University Genome
Sequencing Center Clone distribution: Genome Systems, St. Louis,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pZIPLOX; Site_1: NotI; Site_2: SalI; Original library was constructed in lambdaEIPLOX. resultsion of the cDNA library was performed to yield pZIPLOX plasmids. Insert check was done in original
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/sex="mixed male and female"
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stage whole embryo cDNA library
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Ostariophysi; Cypriniformes
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                              Email: cgapbs-r@mail.nih.gov

Eco RI site shown at the beginning of the sequence.

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

cDNA Library Preparation: M.B. Soares Lab

cDNA Library Arrayed by: M.B. Soares Lab

CNA Library Arrayed by: M.B. Soares Lab

Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:

www-bio.llnl.gov/bbrp/image/image.html

Seq primer: M13 Forward.
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1 (bases 1 to 292)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Contact: Robert Strausberg, Ph.D.
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UI-HF-BROp-ajx-b-11-0-UI.rl NIH_MGC_52 Homo
IMAGE:3075813 5', mRNA sequence.
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Location/Qualifiers
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5' EST sequencing of clones from a zebrafish shield stage library, normalised from 55,000 starting clones by oligonucleotide
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Thnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1562
Fax: +49 30 8413 1380
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/lab_host="E.coli, XLI blue MRF"
/note="Vector: pSport1; Site_1: NotI; Site_2: SalI;
oligo-dT-NotI primed, SalI adaptors, directionally cloned,
library normalised by oligonucleotide fingerprinting"
a 152 c 139 g 139 t 1 others
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/db_xref="taxon:7955"
/db_cxref="taxon:7955"
/clone="MPMGp637_IBE17; MPMGp637E1718"
/clone_lib="Zebrafish shield stage who library MPMGp637"
/tissue_type="whole embryo"
              Location/Qualifiers
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UI-HE-BROp-ajm-g-11-0-UI.rl NIH_MGC_52 Homo sapiens AMSGE:3075260 5′, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW501791.1 GI:7115654
EST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW501791
                                                                                                                                                                                                                                                                                                                found through the I.M.A.G.E. Consortium/LLNL
www-bio.llnl.gov/bbrp/image/image.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 338)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                  Seq primer: M13 Forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
              56
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         /lab_host="DH10B (LTI)" .
/lab_host="DH10B (LTI)" .
/note="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI; /Constructed from size fractionated cytoplasmic mRNA (7.4-9.5kb) . Directionally cloned. Cells provided by Louis M. Staudt, Ph.D. Library preparation by Maria de Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. " 98 c 124 g 60 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone="IMAGE:3075260"
/clone_lib="NIH_MGC_52"
/tissue_type="lymph"
/cell_type="germinal center B cells"
/cell_line="MGC85"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:3075813"
/clone_lib="NIH_MGC.52"
/tissue_type="lymph"
/cell_type="germinal center
/cell_line="MGC85"
                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
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94.4%;
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Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 9;
l.6e+03;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B cells"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 292;
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Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST 01-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Query Match

82.0%;

Score 16.4;

DΒ

9;

Length 338;

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Best Local Similarity, 94.4%; Pred. No. 1.6e-03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Oy 2 acggregagactgatc 19
Db 46 ACCOTCCGCCTTCATC 63

Search completed August 7, 2002, 21:15:21

Job time: 22891 sec
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Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Searched
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     and is derived by a
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    133.88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Issued_Patents_NA:*
1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             length: 0
length: 2000000000
    100.0
100.0
100.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           is the number of results predicted by chance to have a ster than or equal to the score of the result being printed, rived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                          Match
                                                                                                                                                                                                                                                                                                                                                                                                                         Query
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20
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Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   383533 seqs, 122816752 residues
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Copyright (c) 1993 - 2000 Com
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/ina/5A_COMB.seq:*
/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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  432
432
620
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620
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620
706
970
970
1970
1970
1170
1153
2262
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1177
1177
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 US-08-313-185-59
US-08-757-653-135
US-08-757-653-136
US-08-757-653-139
US-08-757-653-139
US-08-757-653-140
US-08-757-653-140
US-08-757-653-140
US-08-757-653-140
US-08-250-0300-1
US-08-620-354-2
US-08-620-354-8878-5
US-08-9372-4488-5
US-08-951-844-5
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33.508 Million cell updates/sec
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Sequence 59, Appl
Sequence 135, App
Sequence 137, App
Sequence 137, App
Sequence 138, App
Sequence 139, App
Sequence 24, Appl
Sequence 21, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 57, Appl
Sequence 57, Appl
Sequence 2, Appl
Sequence 2, Appl
Sequence 3, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 9, Appl
Sequence 5, Appl
Sequence 6, Appl
                                                                                                                                                                                                                                                                                                                                                                                                          Description
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; MOLECULE TYPE: US-08-313-185-59

DNA (genomic)

Query Match

100.0%;

Score

20;

DB 2;

Length 432;

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RESULT 1
US-08-313-185-59/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 59, Applicat Patent No. 5851763 GENERAL INFORMATION:
                                                                                                     COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Vei
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068
                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 408-4000
TELEPAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                     APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Douglas
APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Tolenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: In Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatil
                                                                                                                                                                                                                                                                              ADDRESSEE: Finnegan, Hender
ADDRESSEE: Dunner
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9, Application 5851763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Finnegan, Henderson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 US-09-103-840A-2
US-09-404-671-3
US-09-372-422A-45
US-08-998-416-705
US-08-9177-234-7
US-09-372-422A-29
US-08-314-309A-2
US-08-314-309A-2
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US-09-479-409-34
US-09-479-453-37
US-09-372-422A-39
US-09-372-624-1
US-09-271-064-1
US-09-271-053-29
US-09-479-409-29
US-09-479-409-29
US-09-479-409-29
US-09-479-409-29
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                                                                                                                                                                                                 Version
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Sequence 34, Appl
Sequence 37, Appl
Sequence 37, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 29, Appli
Sequence 29, Appli
Sequence 29, Appli
Sequence 27, Appli
Sequence 37, Appli
Sequence 45, Appli
Sequence 705, Appli
Sequence 705, Appli
Sequence 705, Appli
Sequence 7, Appli
Sequence 29, Appli
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RESULT 3
US-08-757-653-135/c
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; Sequence 59, Application US/09082614A
Sequence 135, Application US/08757653 Patent No. 5843669
                                                                                                                                                                                                                                                                                                                                       TELEFAX: (202) TO SECULATION FOR SEQ ID NO: 59
INFORMATION FOR SEQ ID NO: 59
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
1 PNGTH: 432 base pairs
1 PNGTH: 432 base pairs
                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                              Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 0:
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Reli
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
                                                                                                        428 TACGGCGTTTCGATGAACCC 409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Young, Douglas
APPLICANT: Zhang, Ying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
COUNTRY: USA
TTP: 20005-3315
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                                                                                                                                                                                                                                                                                                      STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1300 I St
CITY: Washington
                                                                                                                         1 tacggcgtttcgatgaaccc 20
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ADDRESSEE: Dunner
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                                                                                                                                                                              Conservative
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                                                                                                                                                                                           100.0%; Score 20; DB 3; 100.0%; Pred. No. 0.033;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 08/313,185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US/09/082,614A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 0.033;
); Mismatches
                                                                                                                                                                             Mismatches
                                                                                                                                                                                                              DB 3; Length 432;
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                                                                                                                                                                             Indels
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RESULT 4
US-08-757-653-136/c
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                                                                                                                                                                                                                                                                                                                                           Sequence 136, Application US/08757653 Patent No. 5843669
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (415) 397-83 INFORMATION FOR SEQ ID NO:
        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                    APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
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ADDRESSEE: Medlen & Carroll, LLP
                                                                                                                                                                                                                                                                                                         APPLICANT: Kaiser, Michael W.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Medlen & Carroll, II
STREET: 220 Montgomery Street,
CITY: San Francisco
STATE: California
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CITY: San Francisco
                                                                                                   ZIP:
                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
les 20; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/757,653 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: double
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                                                                                                                  United States
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397-8338
15 NO: 135:
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                   Suite 2200
                Version #1.30
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APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435

US/08/757,653

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                                                                                                              REGISTRATION NUMBER: FORS-
REFERENCE/DOCKET NUMBER: FORS-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEPHAX: (415) 397-8338
TELEPHAX: 150 110 NO: 137:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                  TELEFAX: (415) 397-833
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
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                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
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    MOLECULE TYPE:
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STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                    TOPOLOGY:
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                                       STRANDEDNESS:
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                                                                               ENGTH:
                                                        nucleic acid
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                    linear
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DNA (genomic)
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3ER: FORS-02565
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US-08-757-653-138
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TELEPHONE: (415) 705-8410
TELEPAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 138:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity
                                                                                                                 Sequence 1 Patent No.
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                                                                                                                                                                                                                                                                                                   Best Local
                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                 GENERAL INFORMATION:
                           APPLICANT: Kaiser, Michael W. APPLICANT: Lyamichev, Victor I. APPLICANT: Lyamichev, Victor I. APPLICANT: Lyamichev, Lacisha TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Cleavage of nucleases TITLE OF INVENTION: Thermostable FEN-1 Endonucleases Number OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
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               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 TACGGCGTTTCGATGAACCC 277
                                                                                                                                                                                                                     325 TACGGCGTTTCGATGAACCC 344
                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
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Lyamichev, Natasha
IVENTION: Cleavage Of Nucleic Acid Using
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ilarity 100.0%;
Conservative (
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Thermostable FEN-1 Endonucleases 190
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Pred. No. 0.034;
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

San Francisco

E: Medlen & Carroll, LLP 220 Montgomery Street, Suite 2200

California

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                                                                         GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 620 base pairs
TYPE: nucleic acid
        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,0
                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll, LLP
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                  APPLICANT: Kaiser, Michael W.
APPLICANT: Lyamichev, Victor I.
APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
NUMBER OF SEQUENCES: 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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ZIP: 94104
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REFERENCE/DOCKET NUMBER: FORS-02565
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CLASSIFICATION: 435
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NUMBER:
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FORS-02565
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Pred. No. 0.034;
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US-08-797-812-24/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                    APPLICATION NUMBER: US/08/797,812
FILING DATE: 07-FEB-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,765
FILING DATE: 15-MAY-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/629,031
FILING DATE: 08-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/012,631
FILING DATE: 01-MAR-1996
PRIOR APPLICATION NUMBER: US 60/012,631
FILING DATE: 01-MAR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
NAME: Fitts, Renee A.
REGISTRATION NUMBER: 15,136
REFERENCE/DOCKET NUMBER: 1652
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
APPLICANT:
                                                                                                 ATTORNEY/AGENT INFORMATION: NAME: Fitts, Renee A.
                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Chip-Based Species Identification and TITLE OF INVENTION: Phenotypic Characterization of Microorganisms NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
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                                                                                                                                    APPLICATION NUMBER: US 60/011,339 FILING DATE: 08-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94111
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CA
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Chee, Mark S.
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Pred. No. 0.034;
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; MOLECULE TYPE: US-08-797-812-24
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              RESULT 11
PCT-US95-06790-1/c
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US-08-250-030-1
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APPLICANT: PETSING,
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
Sequence 1, Application PC/TUS9506790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 100.0%; Score 20; DB 4; Best Local Similarity 100.0%; Pred. No. 0.035; Matches 20; Conservative 0; Mismatches
                                                                                                                                                        Query Match
Best Local
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                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                  TELEFAX: 612-339-3061 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/250,030
FILING DATE: 26-MAY-1994
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 706 base pairs
TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION: NAME: Mueting, Ann M.
                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                              671
                                                                                                                                                                                                                                                                                                                                                                                               NAME: Mueting, Ann M.
REGISTRATION NUMBER: 33,977
REFERENCE/DOCKET NUMBER: 15
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                                                                                                                                           Local Similarity
nes 20; Conserv
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                                                                             ENGTH:
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                                                                                                                                                                                                                                                                                    nucleic acid
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3500 IDS Center
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Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Detection of a Genetic Locus Encoding Resistance to Rifampin in Mycobacterial Cultures
                                                                             652
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                                                                                                                                                       Score 20; DB 1;
Pred. No. 0.036;
                                                                                                                                          Mismatches
                                                                                                                                                                       DB 1;
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; MOLECULE TYPE:
PCT-US95-06790-1
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                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                        APPLICANT: DE BEENHOUWER,
APPLICANT: PORTAELS, FRAN
APPLICANT: MACHTELINCKX, L
APPLICANT: JANNES, GEERT
APPLICANT: ROSSAU, RUDI
                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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ZIP: 20005-3934

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                               NUMBER OF SEQUENCES: 7.
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERNE, K.
STREET: 1100 NEW YOR
                                                                                                                                                                                                                                        TITLE OF INVENTION:
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LENGTH: 970 base pairs
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FILING DATE: 26-MAY-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TITLE OF INVENTION: Detection of a Genetic Locus Encoding TITLE OF INVENTION: Resistance to Rifampin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                671 TACGGCGTTTCGATGAACCC 652
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Raasch, Kevin W. REGISTRATION NUMBER: 35 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                  CITY: WASHINGTON
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                                                                                                                COUNTRY:
                                                                                                                                   STATE:
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                                                                                                                                                                 EE: STERNE, KESSLER, GOLDSTEIN & 1100 NEW YORK AVENUE, SUITE 600
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PORTAELS, FRAN OISE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                      METHOD FOR DETECTION OF THE ANTIBIOTIC RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES
                                                                                                                                                                                      KESSLER, GOLDSTEIN & FOX P.L.L.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PCT/US95/06790
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CURRENT APPLICATION DATA:

21-FEB-1997

US/08/750,088A

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RESULT 13
US-08-313-185-57/c
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                                                                                                                                                                             ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: PAtentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/313,185

FILING DATE: 12-OCT-1994

CLASSIFICATION: 435
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Best Local S
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TELERA: (202) 408-4400
INFORMATION FOR SEQ ID NO: 57:
SEQUENCE CHARACTERISTICS:
LENGTH: 3447 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 29,021
REFERENCE/POCKET NUMBER: 1657.0010000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEPAX: 202-371-2540
                                                                         TELEPHONE: (202) 408-4000
                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                           COUNTRY:
ZIP: 200
                                                                                                         NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02
                                                                                                                                                                                                                                                                                                                                                                     STREET: 1300 I STREET: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: STRANDEDNESS: SIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 21-FER CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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1300 I Street, N.W.
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Cole, Stewart
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Zhang, Ying
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1 tacggcgtttcgatgaaccc 20

Matches

Similarity 95. 19; Conservative

0

Mismatches

Indels

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Gaps

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; STRANDEDNESS: single; TOPOLOGY: linear; MOLECULE TYPE: DNA (gen US-09-082-614A-57
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US-09-082-614A-57/c
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 Query Match
Best Local :
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Best Local
                                                                                                                                                                      TELEFAX: (202) 408-440 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1454 TACGGTGTTTCGATGAACCC 1435
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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CITY: Washington
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ADDRESSEE: Dunner
ADDRESSEE: 1300 I Street, N.W.
                                                                                                                                    TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0
                                                                                                                                                                                                                                                                        NAME: Meyers, Kenneth J. REGISTRATION NUMBER: 25,146
                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 / Match 92.0%;
Local Similarity 95.0%;
nes 19; Conservative
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Zhang, Ying
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                                                                                    DNA (genomic)
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92.0%;
95.0%;
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Score 18.4; DB Pred. No. 0.32;
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Pred. No. 0.32;
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                DB 3; Length 3447;
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1454 TACGGTGTTTCGATGAACCC 1435

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COUNTRY: VA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/622,354
FILING DATE: 27-MAR-1996
CLASSIFICATION: 435
ANTORNEY/AGENT INFORMATION:
NAME: Price, Robert L.
REGISTRATION NUMBER: 22,685
REFERENCE/DOCKET NUMBER: 434-061
TELECOMMUNICATION INFORMATION:
TELEPAX: (703) 684-1114
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1472 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
FFATURE:
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US-08-622-354-2/c
US-08-622-354-2/c
; Sequence 2, Application US/08622354
; Patent No. 5827518
; Patent No. 5827518
; GENERAL INFORMATION:
                                                                                                                                              ş
                                                                                                                                                                                                                                                                                            ; NAME/KEY:
; LOCATION:
US-08-622-354-2
Search completed: August 7, 2002, 21:54:21 Job time: 24016 sec
                                                                                                         망
                                                                                                                                                                                     Query Match 79.0%; Score 15.8; I Best Local Similarity 89.5%; Pred. No. 8; Matches 17; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: WEBB, Bruce A.
APPLICANT: WEBB, Bruce A.
APPLICANT: CUI, LIWANG
TITLE OF INVENTION: VIRAL AND INSECT GENES THAT INHIBIT THE
TITLE OF INVENTION: IMMUNE SYSTEM AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSE: LOWE, PRICE, LEBLANC & BECKER
STREET: 99 Canal Center Plaza, Suite 300
CITY: Alexandria
STATE: VA
                                                                                                    1105 TACGGGGTTTAGATGAACC 1087
                                                                                                                            1 tacggcgtttcgatgaacc 19
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190..1155
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Result
No.
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Maximum DB seq length: 2000000000
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Perfect score:
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                             Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Ouery
O. Score Match
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1: gb_ba:*
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12:
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Gapop 10.0 , Gapext 1.0
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Listing first 45 summaries
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193.058 Million cell updates/sec
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F173086 Mycob	73084 Mycobact	F057495 Nocardi	AF057494 Rhodococ	057492 Mycobact	F057489 Mycobact	F057480 Mycobact	57475 Mycobac	F057466 Mycobact	F057463 Mycobact	X050338 Sequenc	157046 Sequenc	R157024 Sequenc	157021 Sequenc	R157011 Sequenc	R157010 Sequenc	157005 Sequenc	173087 Mycobact	F057496 Coryneba	F057473 Mycobact	57471 Mycobact	F05746	F05745	05745	47816 Sequence 3	R15704	F05749	95972	00696	L27989	12205	1339	50706 9	R067448	05910	R157051	R157042	R157008	R157007	157003	F057454	F057453	F05745	AF057451 Mycobacte	F057450	

ALIGNMENTS

RESULT 1
AF057450
LOCUS
AF057450
AF057450
Mycobacterium africanum RNA polymerase beta (rpoB) gene, partial cds.
ACCESSION AF057450
VERSION AF057450.1 GI:5902487
KEYWORDS
SOURCE Mycobacterium africanum.
ORGANISM Mycobacterium africanum.
Bacteria: Firmicutes: Actinobacteriaeae; Mycobacterium: Mycobacterium tuberculosis complex.
Actinomycetales: Corynebacterineae: Mycobacteriaeae; Mycobacterium: Mycobacterium tuberculosis complex.

REFERENCE 1 (bases 1 to 306)
AUTHORS Kim,E.C., Cha,C.Y. and Kook,Y.H.
TITLE Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
JOURNAL J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
REFERENCE 2 (bases 1 to 306)
REFERENCE 2 (bases 1 to 306)
AUTHORS Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H.,

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PUBMED
REFERENCE
AUTHORS
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AF057451
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Best Local S
Matches 20
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JOURNAL
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JOURNAL
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Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,

Kim,E.C., Cha,C.Y. and Kook,Y.H.

Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)

J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (06-APR-1998)
College of Medicine, 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kim,
                                                                                                                                                                                 Submitted (06-APR-1998) Microbiology, Seoul National University College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799
                                                                                                                                                                                                               (bases 1 to 306)

Kook, Y.H., Kim, B.J., Lee, S.H.,

Kim, S.J., Chae, G.T., Kim, E.J. &

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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VVAAIKEFGTSOLSOFMDQNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHPSH"
05 c 108 g 47 t
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<1. .>306
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                       .>306
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Pred. No.
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and Cha, C.Y.
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Mycobacterium bovis BCG.
Bycobacterium bovis BCG.
Bacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bal,G.H., Chae,G.T., Kim,E.C., Cha,C.Y. and Kook,Y.H.
Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
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                                             Similarity 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (06-APR-1998) Microbiology, Seoul National University College of Medicine, 28 Youngon-dong, Chongno-gu, Seoul 110-799,
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                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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In French 1173P2 RNA polymerase
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AF057453.1
Mycobacterium tuberculosis.

Mycobacterium tuberculosis.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;

Mycobacterium; Mycobacterium tuberculosis complex.
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Mycobacterium tuberculosis RNA
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Rook, Y. H., Kim, B. J., Lee, S. H., Lyu, M.A., Kim, S. J., Kim, S. J., Chae, G. T., Kim, E. J. and Cha, C. Y.

Direct Submission

Submitted (06-APR-1998) Microbiology, Seoul National College of Medicine, 28 Youngon-dong, Chongno-gu, 1
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Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
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1 (bases 1 to 306)
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Identification of mycobacterial species by canalysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
                                                                                                                                                                            Method for identifying mycobacterial sequence analysis of rpoB gene Patent: US 6242584-A 2 05-JUN-2001;
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Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
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/protein_id="AAD55518.1"
/db_xref="G1:5902496"
/translation="RTYGELIQNQIRVGMSRMERVVRERMTTQDVEATTPQTLINIRP
/translation="RTYGELIQNQIRVGMSRMERVVRERMTTQDVEATTPQTLINIRP
VVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHPSH"
vvaaikeffgtsqlsqfmdqnnpLsglthkrrlsalgpgglsreraglevrdvhpsh"
vpaikeffgtsqlsqfmdqnnplsglthkrrlsalgpgglsreraglevrdvhpsh"
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/strain="H37Rv; ATCC27294"
/db_xref="ATCC:27294"
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Kook, Y.-H. and Kim, B.-J.
Method for identifying mycobacterial species by comparative sequence analysis of rpoB gene patent: US 6242584 A 6 05-JUN-2001;
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Kook, Y. and Kim, B.

Method for identifying mycobacterial species by comparative sequence analysis of rpoB gene patent: US 6242584-A 41 05-JUN-2001;
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                                                                                                                                                         Mycobacterium tuberculosis RNA polymerase beta resistance gene, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                               Method for identifying mycobacterial species sequence analysis of rpoB gene Patent: US 6242584-A 50 05-JUN-2001;
                                 Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 432)
Telenti,A., Imboden,P., Marchesi,F., Lowrie,D., Cole,S.T., Colston,J., Matter,L., Schopfer,K. and Bodmer,T.
                                                                                                        RNA polymerase beta-subunit; rifampicin resistance. Mycobacterium tuberculosis (strain H37) DNA. Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kook, Y. and Kim, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unclassified
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          tuberculosis
                         Detection of rifampicin-resistance
                                                                                                                                                L05910.1 GI:149991
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50 from patent US 6242584.
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95 c 108 g
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1. .306
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94 c 108 g
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Section 15

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TACGGTCGGCGAGCTGATCC
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INIRVVAAIKEFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDV
HPSHYGRMCPIETPEGPNIGLIGSLSVYARVNPFGFIETPYR"
                                                                                                                                                           /phenotype="rifampicin
/replace="t"
254
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/replace="ca"
248
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/replace="g"
233
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/replace="a"
233
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mutation 203 T"
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194
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mutation 234 G"
/replace="c"
188
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/replace="c"
140 c 148 g
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247. .248
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/replace=""
232
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208. 210
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/strain="H37"
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/protein_id="AAB59068.1"
/db_xref="GI:149992"
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/transl_table=11
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/replace="g"
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RESULT 12
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Sequence
AX111339
                                                                                                                                                   th 100.0%; Similarity 100.0%; 20; Conservative (
                                                                                                                                                                                                                                               Detection of a genetic locus encoding resistance mycobacterial cultures and in clinical specimens Patent: US 5643723-A 1 01-JUL-1997;
Location/Qualifiers
                                                                                                                                                                                                                                                                                         1 (bases 1 to 970)
Persing,D.H., Hunt,J.J.,
and Whelan,A.Christian.
                                                                                                                                                                                                                                                                                                                                                                                Sequence 1 from 150706
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Heym, B., Cole, S., Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown
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AR067448
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 Mycobacterium tuberculosis
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139 c 149 g
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1. .432
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302 c 330 g
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                      GI:13927631
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from patent US 5851763.
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                                          3534 bp
from Patent WO0123604
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                                                      PAT 30-APR-2001
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 3534)
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Imboden,P., Troller,R., Marchesi,F., Telenti,A., Cole,S., Schopfer,K. and Burkart,T.
The rpoB gene of Mycobacterium tuberculosis
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Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpob)
gene, partial cds.
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                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (11-JUL-1994) Paul Imboden, Institute for Medical Microbiology, University of Berne, Friedbuehlstrasse 51, Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium; Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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Picard,F.J. and Roy,P.H.
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1081 c 1188 g
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EEDVVATIEYLVRLHEGQTIMTVPGGVEVPVETDDIDHFGNRRLRTVGELIQNOIRVG
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TIKS"

1173 c 1293 g 664 t
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B Ş Matches Query Match Best Local Similarity Conservative 100.0%; 0; Score 20; Pred. No. Mismatches Ξ. 0 Length 3853; Indels 0; Gaps

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Search completed: August 7, 2002, 21:51:38 Job time: 23873 sec

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Post-processing: Minimum Match 0%
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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ALIGNMENTS

REFERENCE AUTHORS TITLE JOURNAL ACCESSION VERSION KEYWORDS RESULT BF220419 LOCUS SOURCE ORGANISM FEATURES COMMENT DEFINITION source North Carolina State University Tel: 919 515 7800 Fax: 919 515 7801 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; 1 (bases 1 to 396) BF220419 BF220419.1 GI:11126551 EST. BF220419 396 bp NXCI_146_A06_F NXCI (Nsf Xylem taeda cDNA clone NXCI_146_A06 9 Unpublished (2000) Contact: Johnson, Arthur Pinus taeda Sederoff, R. Molecular Basis of Wood Formation loblolly pine. ull: ajohnson@unity.ncsu.edu primer: T3. /clone="NXCI_146_A06"
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: The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form
compression wood by bending to a 45 degree angle and tying
them to the ground. Differentiating xylem was harvested
from the bottoms of the inclined stems, and a mixture of /organism="Pinus taeda" /strain="Coastal plain loblolly pine from North Carolina" /db_xref="taxon:3352" Location/Qualifiers . 396 396 bp 5′, Compression wood ', mRNA sequence. 'n mRNA the Pine Megagenome linear Inclined) Pinus EST 08-NOV-2000 Tracheophyta; Pinus; Pinus.

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BF169611
BF169611.1 GI:11054228
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Seq primer: T3.
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Tel: 919 515 7800
Fax: 919 515 7801
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecular Basis of Wood Formation in Unpublished (2000)
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Spermatophyta; Coniferopsida;
1 (bases 1 to 399)
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                                                          Conservative
                                                                                                                                                                      /note="vector: BlueScript SK; Site_1: Eco RI; Site_2: XhoI
; The library is from early (spring) wood, taken from
three six-year old trees (three different genotypes), in
the juvenile phase. These trees were induced to form
compression wood by bending to a 45 degree angle and tying
them to the ground. Differentiating xylem was harvested
from the bottoms of the inclined stems, and a mixture of
all three genotypes was used for the library. oligo-dT
primed cDNA was directionally cloned into the EcoRI-XhoI
BlueScript SK vector arms. NOTE: The sequences contain a
'CDNA adapter' between the EcoRI site and the start of the
EST. The adapter sequence is 'AATTCGGCACGAG'."

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Pred. No. 72;
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452 bp mRNA linear EST 24-JAN-2001

NXSI_110_F06_F NXSI (Nsf xylem Side wood Inclined) Pinus taeda cDNA

colone NXSI_110_F06 5', mRNA sequence.
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North Carolina State University
Tel: 919 515 7800
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 539)
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//lab.host="XLI-Blue"
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/clone_lib="NXSI (Nsf Xylem
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/db_xref="taxon:3352"
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                                                                                                                                                                                   North Carolina State University Tel: 919 515 7800 Fax: 919 515 7801
                                                                                                                                                                                                                                              Unpublished (2000)
Contact: Johnson, Arthur
                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus; Pinus. 1 (bases 1 to 545)
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North Carolina State University
Dept. of Forestry, NC State University,
NC, 27695-8008
                                                                                                                                              Email: ajohnson@unity.ncsu.edu
Seq primer: T3.
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, Retzel, E. Campbell, M.M., Sederoff, R. and Whetten, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Vector: lambda-ZAP; Site_1: ECORI; Site_2: XhOI; The result of subtraction of C library th N library. Immature xylem from the underside of inclined stems of differentiating compression wood was subtracted with Immature xylem from the side of inclined stems of differentiating wood. A mixture of four genotypes were used. Oligo-dT primed cDNA was directionally cloned into the ECORI-XhOI lambda-ZAP vector arms."
/organism="Pinus taeda"
/strain="Coastal plain loblolly pine from North Carolina"
/db_xref="taxon:3352"
/clone="wxsI_066_ED5"
/clone_lib="wxsI (Nsf Xylem Side wood Inclined)"
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/tissue_type="Xylem"
/lab_host="SOLR"
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/db_xref="taxon:3352"
/clone="1CAB46"
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KEYWORDS
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: (5531)4415611
Fax: (5531)4415409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     W06754.1 GI:1444974
EST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Franco,G.R. Franco,G.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Platyhelminthes; Trematoda; D
Strigeidida; Schistosomatoidea; Schistosomatidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schistosoma mansoni
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 234)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                primer: M13 Forward
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//dev_Stage="Juvenile"
//lab_host="%K1-Blue"
//note="vector: BlueScript SK; Site_1: Eco RI; Site_2: xhoI
/*note="vector: BlueScript SK; Site_1: xhoI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gfranco@mono.icb.ufmg
Note="Vector: BA vector; Site_1: NotI; Site_2: HindIII; Total cellular RNA from male and female adult worms was extracted according to a modification (Puissant, C. and Houdebine, L. M. BioFeedback 8, 148-149, 1990) of the Guanidine Thiocyanate procedure (Chomczynski, P. and Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+RNA was purified by oligo dT column and cDNA was synthesized as described previously (Adams, M. D. et al. Nature Genet. 4, 373-389, 1993). cDNA was ligated to a
                                                                                                                                                                                                                                                                                                                                                   Franco"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Schistosoma
/strain="NMRI"
                                                                                                                                                                                                                                                                                                             /lab_host="DH10B, JM109"
                                                                                                                                                                                                                                                                                                                                                                                                              /clone-"SMPBE73"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:6183"
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/cell_type="Side"
                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Schistosoma mansoni, adult worm, Gloria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and Pena, S.D.J., Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          87.08;
94.78;
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Pred. No. 78;
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stosomatidae; Schistosoma.
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Gloria Franco
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17; Conserv
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Identification of new Schistosoma mansoni genes using a directional cDNA library Gene 152, 141-147 (1995)

95137379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMEST0325 Schistosoma mansoni, adult worm, Gloria Franco Schistosoma mansoni cDNA clone SMPBC65 3', mRNA sequence.
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Fax: (5531)4415409
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/lab.host="DH10B, JM109"
/lab.host="DH10B, JM109"
/lab.host="DH10B, JM109"
/lab.host="DH10B, JM109"
/lab.host="DH10B, Vector; Site_1: Not1; Site_2: HindIII;
/note="Vector: BA vector; Site_1: Not1; Site_2: HindIII;
/note="Vector: BA vector; Site_1: Not1; Site_2: HindIII;
/note="Vector: BA vector was and female adult worms was
extracted according to a modification (Puissant, C. and
Houdebine, L. M. BioFeedback 8, 148-149, 1990) of the
Guanidine Thiocyanate procedure (Chomczynski, P. and
Sacchi, N. Anal. Biochem. 162, 156-159, 1987). Poly (A)+
RNA was purified by Oligo dT column and cDNA was
synthesized as described previously (Adams, M. D. et al.
Nature Genet. 4, 373-389, 1993). cDNA was ligated to a
two fold molar excess of a NotI/HindIII digested plasmid
DNA (lafmid BA vector, a phagemid derived from pEMBL,
Adams, M. D. et al. Nature Genet. 4, 373-389, 1993)) and
electroporated into E. coli strain DH10B (BRL). The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Schistosoma
/strain="NMRI"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:6183"
/clone="SMPBC65"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Schistosoma mansoni, adult worm, Gloria
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Adams, M.D., Soares, M.B., Simpson, A.J.G., Venter, J.C.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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adult wor
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1e+02;
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Gloria Franco
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MG
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REFERENCE

TITLE AUTHORS

JOURNAL

SOURCE

KEYWORDS VERSION ACCESSION

COMMENT

FEATURES

ORIGIN

멍 Q

Matches

T24127/c RESULT ORIGIN BASE COUNT

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RESULT
AA734164
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuc
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylle,T., Lennon,G., Soares,B., Wilson,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Marra M/Mouse EST Project
Washington University School of Medicinep
4444 Forest Park Parkway, Box 8501, St. Lo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mus musculus
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AA734164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unpublished (1996)
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       64
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a 206 c 179 g 88 t 4 others
                                                                                                                                                                            /note="Vector: pT7T3D-Pac (Pharmacia) with a modified /note="Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: EcoRI; Site_2: NotI; Tissue obtained from 8 week old mouse. Colon was harvested 72 hours after irradiation with 1400 Gys. 1st strand cDNA was primed with a Not I - oligo(dT) primer tolly color tolly col
                                                                   T 3']; double-stranded cDNA was ligated to Eco adaptors [AATTCGGATCCTTG], digested with NOT I into the Not I and Eco RI sites of the modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:1138726"
                                         vector.
                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="Barstead mouse irradiated colon MPLRB7"
/dev_stage="8 weeks"
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100.0%;
   Library constructed by Bob Barstead.
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Pred. No.
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MPLRB7 Mus musculus cDNA
9 M.musculus L26 mRNA
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Matches 17
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1 (bases 1 to 576)
Gardner, M.J. and Kirkland, T.
Generation of ESTs from Coccidioides immitis spi
            NIH-MGC http://mgc.nc1.nih.gov/.
National Institutes of Health, M
                                                      Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
                                                                                                              EST
                                                                                                                                        mRNA sequence.
BE896357
                                                                                                                                                                BE896357 624
601439015F1 NIH_MGC_72 Homo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Malcolm J. Gardner
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville,
Tel: 301 838 3519
Fax: 301 838 0208
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                                                                                   Homo sapiens
                                                                                                                          BE896357.1 GI:10360678
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                                           (bases 1 to 624)
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Location/Qualifiers
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/dev_stage="spherule"
/lab_host="SOLR"
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/db_xref="taxon:5501"
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xho1"
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Pred. No. 1.
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IMAGE:3924266 5',
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High quality sequence stop: 403.
                                   Seq pri
Class:
                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Blaxter ML
Institute of Cell, Animal and Population
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BH615799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BH615799 631 bp DNA linear (BMBAC304F01SP6_PSU Brugia malayi Genomic Bac Library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies,
cDNA Library Arrayed by: The I.M.A.G.E. Conso
                                                                                    Email: mark blaxter@ed.ac.uk
Sequenced from the Brugia malayi BAC library constructed by Claire
Whitton and Dr Mike Quail. The sequence was generated by The
Pathogen Sequencing Unit, The Sanger Institute, Cambridge, UK in
collaboration with Mark Blaxter, ICAPB, University of Edinburgh,
                                                                                                                                                                               Tel: +44 131 650 6760 Fax: +44 131 670 5450
                                                                                                                                                                                                                                    University of Edinburgh
Ashworth Labs, King's Buildings,
                                                                                                                                                                                                                                                                                                                              marayı
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1 (bases 1 to 631)

1 (bases 1 to 631)

Whitton, C., Daub, J., Ware, J., Quail, M., Hall, N., Barrell, B., Foster, J., Guiliano, D., Slatko, B. and Blaxter, M.
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                                                                                                                                                                                                                                                                                                                                               Genome survey sequences
                                                                         Edinburgh, UK.
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Clone distribution: MGC clone distribution information can
                                   primer: SP6 (ATTTAGGTGACACTATAG)
ss: BAC ends.
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/clone_lib="NIH_MGC_72"
/clone_lib="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1:
/site_2: Sal1; Cloned unidirectionally. Primer: O
Average insert size 2 kb. Library constructed b
Technologies."
                Location/Qualifiers
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/db_xref="taxon:9606"
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/organism="Brugia malayi"

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                                                                                                                                                                                                                                                                                                                                                                                           Submitted (02-AUG-2001) Asao Fujlyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:chimpbes@gsc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9111, Fax:81-45-503-9170)
Tel:81-45-503-9111, Fax:81-45-503-9170
Clones are derived from the chimpanzee BAC library RPCI-43 This BAC end was generated during the R&D process and may have higher chance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         sequence.

AG141490
AG141490.1 GI:16671168
AG141490.1 GI:16671168
GSS; GSS (genome survey sequence).
GASS; GSS (genome survey sequence).
GASS; GSS (genome survey sequence).
GASS; GSS (genome survey sequence).
Fan troglodytes male lymphocytes DNA, clone_lib:RPCI-43 Chimpanzee
Male BAC Library clone:RP43-001J13.TJ.

Pan troglodytes
                                                                                                                                                                                                                                                                                                                                                                          of clone tracking errors.
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Totoki,Y., Watanabe,H. and Sakaki,Y.
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Totoki, Y., Watanabe, H. and Sakaki, Y.
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/sex="Mixed (male and female)"
/tissue_type="whole parasite"
/dev_stage="microfilaria (LL)"
/note="Vector: pBACe3 6; Site_1: BamH I; Brugia malayi
/note="Vector: pBACe3 6; Site_1: BamH I; Brugia malayi
/genomic DNA was partially cleaved with Sau3A I and size
fractionated 7,392 clones were generated with mean insert
size -48 kbp. The library was constructed by Claire
whitton, Blaxter Nematode Genetics Lab, University of
Edinburgh, UK, and Dr Mike Quail, The Pathogen Sequencing
Unit, The Sanger Centre, Cambridge, UK."
96 a 94 c 142 g 199 t
                          മ
                     /cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee
299 c 145 g 252 t
                                                                                                              /organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-001J13.TJ"
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                                                                                           /sex="male"
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436 bp mRNA linear EST 30-NOV-2001 sb05b08.yl Gm-c1004 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1004-7888 5' similar to TR:Q92388 Q92388 CRG1 GENE. ;, mRNA
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17; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene expression profile and identification of differentially expressed transcripts during human intrathymic T-cell development by cDNA sequencing analysis Genomics 70 (1), 1-18 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Korea Research Institute
Oun-dong 52, Yu Sung-Gu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria; Primates; Catarrhini; H
1 (bases 1 to 213)
Goh,S.-H., Park,J.-H., Lee,Y.J., Lee,H.G.,
Park,J.-H., Kim,Y.-S. and Lee,C.-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tel: 82-42-860-4473
Fax: 82-42-860-4479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Sung-Ho Goh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
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                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gohsh@mail.kribb.re.kr
                                                                                                                                                                                                                                                                           /note="Vector: pGEM-T; cDNA was made from total cytoplasmic RNA of sorted human intrathymic CD3+4+8-T-cell, adaptor ligated, amplified with PCR, and clon into pGEM-T vector."

1 59 c 72 g 40 t
                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Thymus"
/cell_type="Intrathymic T-cell"
/dev_stage="CD3+4+8-single pos"
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                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 4
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Daejon 305-333, Republic of Korea
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This clone is available through: ResGen, Invitrogen Corp. 2130
South Memorial Parkway Huntsville, AL 35801 For further information
call: (800)-533-4363 or contact via email: ccu@resgen.com
Seq primer: -40RP from Gibco
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Tel: 314 286 1800
Fax: 314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V., Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C. Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
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         And the second color of pages of the second color of Bady old 'williams' seedlings which were propagated on paper towels with distilled water. Stratagene's color of Bady old 'williams' seedlings which were propagated on paper towels with distilled water. Stratagene's color of the color of t
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/lab_host="xL10-Gold"
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/clone_lib="Gm-c1004"
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/db_xref="taxon:3847"
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Query Match Best Local Similarity

79.0%;

Score 15.8; DB 9; Pred. No. 5.3e+02;

Length 436;

Search completed: August Job time: 22890 sec

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AUTHORS
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                                                       17; Conserv
                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-FEB-2000) Genoscope - Centre National de Seque
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.
- Web : www.genoscope.cns.fr)
2 (bases 1 to 582)
Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Weissenbach,J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AL147937.1 GI:7006083
GSS.
African malaria mosquito.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNSOIK68 Sambiae GSS SP6 end of clone 16E18 of NotreDamel library from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                              Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H.
Collins and sequenced by Genoscope in collaboration with the
Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genomic survey sequence. AL147937
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Eukaryota; Metazoa
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                                                                                                                                            /clone_lib="NotreDamel"
/note="end : SP6"
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                                                                                                                                                                                                       /strain="PEST"
/db_xref="taxon:7165"
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                                                                                                                                                                                                                                      /organism="Anopheles gambiae"
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segref@genoscope.cns
                                                                                   Length 582;
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1: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1980.DAT:*

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8: /SIDSI/gcgdata/geneseq/geneseqn-embl/NA1987.DAT:*
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Listing first 45 summaries
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Method for the detection and characterization of Mycobacterium tuberculosis with antibiotic resistance in a sample - $$	WPI; 2000-431611/37.	Shipman R;	(VISI-) VISIBLE GENETICS INC.	11-DEC-1998; 98US-0111794.	10-DEC-1999; 99WO-CA01177.	22-JUN-2000.	WO200036142-A1.	Mycobacterium tuberculosis.	88.	Antibiotic resistance; rpoB gene; rifampin resistance; PCR primer;	Mycobacterium tuberculosis rpoB gene amplification primer rpoB-R.	25-SEP-2000 (first entry)	AAA49824;	RESULT 1 AAA49824 D AAA49824 standard; DNA; 20 BP.

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(streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
(ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis.
(These primers can be used in a method for the detection and characterization of M. tuberculosis present in a sputum sample.

The method involves performing a sequencing procedure, with or without prior amplification, to detect the presence of M. tuberculosis, and if present to evaluate the rpoB, katG, rpsL/s12
(and 23S genes for the presence of antibiotic-inducing mutations. If M. tuberculosis is detected, a second sequencing procedure is performed on the sample to evaluate additional genes for the presence of antibiotic resistance-inducing mutations. Genotypic tests are rapid, sensitive and accurate providing information as to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                   Claim 4;
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                                                              Method for the detection and characterize tuberculosis with antibiotic resistance
                                                                                                              WPI; 2000-431611/37.
                                                                                                                                                                     (VISI-) VISIBLE
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                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                     Antibiotic resistance; rpoB gene; rifampin resistance; primer;
                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-3s
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the rpoB gene (see AAA49863). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and
                                                                                                                                                                                                                                  10-DEC-1999;
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The present sequence is

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30-APR-1992;
14-AUG-1992;
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                                                                                          Bodmer T,
Young D,
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                                                                                          Cole S, Zhang Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PCR amplification was used to obtain rpoB genes from rifampicin-resistant Mycobacterium leprae strains. A comparison with the sequence of the rpoB gene from sensitive strains (AAQ51532) reveal mutations in the region encoding amino acids 400-450. The corresp. region was isolated from M.tuberculosis (AAQ61457). A common mutation seen in resistant strains occurs at codon 425 where Ser is substituted, most frequently by Leu.
rpoB (rifampin resistance) gene (bp2161-2640). Amplification cycle sequencing primers (see AAA49823-62) are used for the de and analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isonizzid), oxyR-aph (isonizzid), mabA (isonizzid), rpsL/s12 (streptomycin), 16S/rr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rapid detection of antiblotic resistance in Mycobacteria - esp. isoniazid, rifampicin or streptomycin resistance in tuberculosis by detecting mutation in katG, rpoB or rpsL genes
                                                                                    Disclosure;
                                                                                                           Method for the detection and tuberculosis with antibiotic
                                                                                                                                                                                               (VISI-) VISIBLE
                                                                                                                                                                                                                       11-DEC-1998;
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                                                            sequence is that of the Mycobacterium tuberculosis
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                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tuberculosis rpoB gene (rifampin resistance).
                                                                                                                                                                                                                     98US-0111794.
                                                                                                                                                                                                                                               99WO-CA01177.
                                                                                                                                                                                               GENETICS INC
                                                                                                                                                                                                                                                                                                                           /note= "primer of AAA49823"
372..391
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                             complement(41..60)
                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                   5; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               78 A; 139 C; 148 G;
                                                                                                                                                                                                                                                                                                                      /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                    "primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВÞ
                                                                                                           characterization of Mycobacterium resistance in a sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score
Pred.
                                                                                                                                                                                                                                                                                                                    of AAA49824"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                         rifampin resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
  oxyR-aphC
), 16S/rrs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        revealed
                                     detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
             PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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polymerase, Escherichia cóli ExoIII and the Saccharomyces cerevi: Radl/Radl0 complex. The nucleic acid substrate is preferably an oligonucleotide containing a human p53 gene sequence or alternatively, microbial gene sequences. Cleavage products are

Cleavage of nucleic acids using an enzyme, especially a selected from the group consisting of Cleavase (RTM) By Thermus aquaticus DNA polymerase, Thermus thermophilus

BN

nuclease enzyme, cerevisiae

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 5
AAT29126/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ciprofloxacin) and 23s (azithromycin) genes of M. tuberculosis. These primers can be used in a method for the detection and characterization of M. tuberculosis present in a sputum sample. The method involves performing a sequencing procedure, with or without prior amplification, to detect the presence of M. tuberculosis, and if present to evaluate the rpos, katG, rpsL/s12 and 23s genes for the presence of antibiotic-inducing mutations. If M. tuberculosis is detected, a second sequencing procedure is performed on the sample to evaluate additional genes for the presence of antibiotic resistance-inducing mutations. Genotypic tests are rapid, sensitive and accurate providing information as the state of the sensitive and accurate providing information as
                                                                                                                                                                                                                                                                                                                                                                                                                              rpoB
                                                                                     Example
                                                                                                                               Cleavage
                                                                                                                                                        WPI;
                                                                                                                                                                             Oldenburg
                                                                                                                                                                                                                                    09-MAR-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                          30-AUG-1995;
09-NOV-1994;
                                                                                                                                                                                                                                                                                                                                       WO9615267-A1
                                                                                                                                                                                                                                                                                                                                                                                             p53; mutant;
Escherichia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAT29126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAT29126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibiotic treatment options.
                                                                                                                                                                                                              (THIR-) THIRD WAVE TECHNOLOGIES
                                                                                                                                                                                                                                                                                            09-NOV-1995;
                                                                                                                                                                                                                                                                                                                  23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (streptomycin),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 tacggcgtttcgatgaaccc
                                                                                                                                                        1996-259862/26
                                                                                                                                                                                                                                                                                                                                                                                                                              gene fragment (mutant) from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACGGCGTTTCGATGAACCC 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                        ω
3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                      human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 standard; DNA; 620
                                                                                                                     of nucleic acids to detect mutation(s) - numan p53 gene, to identify strains of mic
                                                                                                                                                                             MC, Olive
                                                                                     Page 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                 mutation; cleavage; nuclease;
Saccharomyces; Campylobacter;
us; identification; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                   95US-0520946.
94US-0337164.
95US-0402601.
95US-0484956.
                                                                                                                                                                                                                                                                                            95WO-US14673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      embB (ethambutol), pncA (pyrazinamide),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89
                                                                                                                                                                             DM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                     433pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           c;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
Pred.
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                                                                                                                                                                                                              INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>و</u>;
                                                                                                                                                                                         Heisler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2
0.38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Η,
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                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                          cleavase; Thermus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                     microorganisms
                                                                                                                                                                                         Lyamichev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 480;
                                                                                                                       allows detection
croorganisms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                                                                                                                                                                             Shigella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT 6
AAT29124/c
ID AAT291
XX AAT291
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XX POB 9
XX POB 9
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XX PS3; m
XW Escher
XW Escher
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XX U7HIR-
XX O14000
XX O14000
XX O14000
XX WPI; 1
XX Cleava
PT Cleava
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PT Cleava
PT Cleava
PT SEAMP1
XX CC Cleava
CC Cleava
CC Cleava
CC Gleava
CC Gligon
CC Gleava
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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-AUG-1995;
09-NOV-1994;
09-MAR-1995;
07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       method is used for detecting mutation in the human p53 gene; for identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter.

Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The method may also be used for the identification of viruses, respecially hepatitis C virus (HCV) and simian immunodeficiency virus (SIV). Two primers (AAT29123, MAT29123) were used to amplify a 620 bp region of the Mycobacterium tuberculosis rpoB gene, which, when mutated is associated with rifampin resistance. The 620 bp region amplified spans both the H451Y and $456L mutations. The amplified
            polymerase, Escherichia coll Exolli und in Complex. The nucleic acid substrate is preferably nationucleotide containing a human p53 gene sequence or containing a huma
                                                                                                                                                Cleavage
                                                                                                                        selected
                                                                                                                                                                                                                                                                                                                                                                                                          Brow MAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23-MAY-1996.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     p53; mutant;
Escherichia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rpoB gene fragment from Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT29124
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      (THIR-) THIRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fragments are given in AAT29124 (Wild type) and AAT29125-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 TACGGCGTTTCGATGAACCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 tacggcgtttcgatgaaccc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . Similarity
20; Conserv
                                                                                             e of nucleic acids using an enzyme, especially a d from the group consisting of Cleavase (RTM) BN aquaticus DNA polymerase, Thermus thermophilus [
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequences).
                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                 human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard;
                                                                                                                                                                                                                                                                                                                                                                                 Dahlberg
MC, Olive
                                                                                                                                                                                                                                                                 f nucleic
nan þ53 ge
                                                                  om the group consisting of Cleavase (RTM) BI
aticus DNA polymerase, Thermus thermophilus
Escherichia coli ExoIII and the Saccharomy
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                                                                                                                                                                                          Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mutation; clear
Saccharomyces;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      WAVE TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    95US-0520946.
94US-0337164.
95US-0402601.
95US-0484956.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          95WO-US14673
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               identification;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    103
                                                                                                                                                                                            305;
                                                                                                                                                                                                                                                              gene,
                                                                                                                                                                                                                                                                 ene, to
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                                                                                                                                                                                                                                                                                                                                                                                 JE,
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                                                                                                                                                                                          433pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Campylobacter;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                       ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                          Heisler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20;
No.
                                                                                                                                                                                                                                                                 mutation(s)
strains of r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 102 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
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                                                                                                                                                                                                                                                                                                                                                                                                       Ĭ,
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                                                                                                                                                                                                                                                                                                                                                                                                       Lyamichev VI;
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                                                                                                                                                                                                                                                                                    allows detection
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                                                                                               DNA
                                                                                                                   enzyme,
                                                                                                                                              nuclease
                                                                       cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     shigella;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          method is used 101 vectors maintains, especially bacteria selected identifying strains of microorganisms, especially bacter, from the the group of members of the genera Campylobacter, Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The method may also be used for the identification of viruses, especially hepatitis C virus (HCV) and simian immunodeficiency virus (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp region of the Mycobacterium tuberculosis rpoB gene, which, when region of the mycobacterium tuberculosis rpoB gene, which, when second and the mycobacterium tuberculosis rpoB gene, which, when region are second and the mycobacterium tuberculosis rpoB gene, which, when the mycobacterium tubercul
                                                                                                                                                                                                                                                                                                                                                                                                           30-AUG-1995;
09-NOV-1994;
09-MAR-1995;
07-JUN-1995;
              selected from the group consisting of Cleavase (RTM) BN enzyme, Thermus aquaticus DNA polymerase, Thermus thermophilus DNA polymerase, Thermus the Saccharomyces cerevisiae polymerase, Escherichia coli ExoIII and the Saccharomyces cerevisiae RadI/RadIO complex. The nucleic acid substrate is preferably an oligonucleotide containing a human p53 gene sequence or
                                                                                                                                                                                                            esp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9125/c
AAT29125
                                                                                                                                                                                                                                                                                                                                  Brow
                                                                                                                                                                                                                                 Cleavage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              гров
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutated is associated with rifampin resistance. The 620 bp amplified spans both the H451Y and S456L mutations. The am fragments are given in AAT29124 (Wild type) and AAT29125-26
                                                                                                                                                                                                                                                                                                            Oldenburg
                                                                                                                                                      Example
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-NOV-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO9615267-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staphylococcus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       p53; mutant;
Escherichia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 620
                                                                                                                                                                                                                                                                                                                                                                         (THIR-) THIRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (mutant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 296
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in
                                                                                                                                                                                                                                                                                                                                  MAD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          is used for detecting mutation in the human p53 gene; for fying strains of microorganisms, especially bacteria selected
                                                                                                                                                      33
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequences).
                                                                                                                                                                                                              human
                                                                                                                                                                                                            of nucleic
human p53 ge
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             to the cleavage products of reference gene sequences.
                                                                                                               of nucleic acids using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; DNA;
                                                                                                                                                                                                                                                                                                              ,
MC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fragment (mutant)
                                                                                                                                                                                                                                                                                                                                  Dahlberg
                                                                                                                                                      Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mutation; cleavage; nuclease;
Saccharomyces; Campylobacter;
us; identification; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BP; 103
                                                                                                                                                                                                                                                                                                              Olive
                                                                                                                                                                                                                                                                                                                                                                         WAVE TECHNOLOGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                           95US-0520946.
94US-0337164.
95US-0402601.
95US-0484956.
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                                                                                                                                                      305-306;
                                                                                                                                                                                                            gene,
                                                                                                                                                                                                                                                                                                                DM;
                                                                                                                                                                                                                                   acids
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                                                                                                               an enzyme,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mycobacterium
                                                                                                                                                                                                                                                                                                                                  Heisler
                                                                                                                                                                                                            mutation(s) - allows detection strains of microorganisms and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20;
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                                                                                                               especially
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                                                                                                                                                                                                                                                                                                                                Lyamichev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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BN
                                                                                                             nuclease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shigella;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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gene sequences

products

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RESULT 8
AAT09676/c
ID AAT09676 standard; DNA; 970 BP
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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    compared to the cleavage products of reference gene sequences. The method is used for detecting mutation in the human p53 gene; for identifying strains of microorganisms, especially bacteria selected from the the group of members of the genera Campylobacter. Escherichia, Mycobacterium, Salmonella, Shigella and Staphylococcus. The method may also be used for the identification of viruses, especially hepatitis C virus (HCV) and simian immunodeficiency virus (SIV). Two primers (AAT29122, AAT29123) were used to amplify a 620 bp region of the Mycobacterium tuberculosis rpoB gene, which, when mutated is associated with rifampin resistance. The 620 bp region amplified spans both the H451Y and S456L mutations. The amplified fragments are given in AAT29124 (Wild type) and AAT29125-26 (mutant sequences).
misc_feature
                                 misc_feature
                                                                   misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                            15-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 100.0%;
l Similarity 100.0%;
20; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                     chain
                                                                                                                                                                                                                                                                                                                                                                                                   disease diagnosis; oligonucleotide; DNA primer;
ain reaction; DNA amplification; rpoB locus; TB;
                                                                                                                                                                                                                                                                                                                                                                                                                                    tuberculosis rpoB gene DNA sequence
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                                                                                               /*tag= g
/note= "M.
433..434
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/note= "primer
348..373
                                 /*tag= 1
/note= "M.
468..469
                                                                  /note= "M.
438
 /note=
486
                                                                                                                                     /note- "primer KY290" 372..373
                                                                                                                                                                      /note- "primer 354..373
                                                                                                                                                                                                                                         /note= "primer 338..364
                                                                                                                                                                                                                                                                          /note= "primer
226..240
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226..243
                     /*tag-
                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                            *tag•
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         tuberculosis signature
                                           tuberculosis
                                                                             tuberculosis signature
                                                                                                              tuberculosis signature nucleotide"
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Pred. No. 0.3
); Mismatches
                                                                                                                                                                               rpo105'
                                                                                                                                                                                                                 rpo95*
                                                                                                                                                                                                                                                    "HDIDD
                                                                                                                                                                                                                                                                                     DDIDHL'
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                                           signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 620;
                                           nucleotide"
                                                                             nucleotide"
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671 TACGGCGTTTCGATGAACCC 1 tacggcgtttcgatgaaccc

652 20 Conservative

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Mismatches

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Gaps

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Query Match
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Matches 20
                                                                     This oligonucleotide DNA primer is specific for Mycobacterium tuberculosis, and may be used to amplify a sample DNA by targeting a portion of the gene encoding rpoB. The 1st several bases comprise nonhybridizing tail consisting of filler bases followed by a restriction site incorporated to facilitate cloning using the amplicon at a later date, if desired. The remaining bases hybridize to bacterial rpoB DNA. The method provides for the detection of M. tuberculosis and the concurrent determination of its drug susceptibility, particularly to rifamycin. The method can provide often greater than 95% sensitivity and 100% specificity. The biological sample is a fluid or tissue sample from a human.
                                                                                                                                                                                                                         Detection of Mycobacterium tuberculosis - by amplifying sample DNA with a primer set that targets portions of the gene encoding rpoB.
                                                                                                                                                                                                                                                           WPI; 1996-030581/03
                                                                                                                                                                                                                                                                                Felmlee TA,
Young KKY;
                                                                                                                                                                                                                                                                                                                                             26-MAY-1994;
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                                                     Sequence 970 BP; 182 A; 302 C; 330 G;
                                                                                                                                                                                                      Disclosure; Fig.3; 54pp; English.
                                                                                                                                                                                                                                                                                                                                                                  26-MAY-1995;
                                                                                                                                                                                                                                                                                                                                                                                                             WO9533074-A1
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                                                                                                                                                                                                                                                                                                                          HOFFMANN LA ROCHE INC
          Similarity
                                                                                                                                                                                                                                                                                                               FOUNDATION.
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                                                                                                                                                                                                                                                                                                                                             94US-0250030
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525.541
/*tag=
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/note= "primer :
640..666
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/note= "N
516..535
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/note=
501
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516
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/note= "primer
952..966
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952..966
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536..562
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                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "primer NMQRQ-2"
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          100.0%;
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           Score 20; DB 1
Pred. No. 0.39;
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                                                                                                                                                                                                                                                                                         DH,
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                                                                                                                                                                                                                                                                                          Roberts GD,
                                                     156 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             signature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          signature
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                    17; Length 970;
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RESULT 1
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ID AAH0
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AC AAH0
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AAH51976/c
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Best Local
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                                                                                                                                                                                                                                                                          polypeptide sequence that may be a drug target, or essential for growth or viability of an organism. Polypucleotide sequences AAH51947 - AAH52092 represent DNA encoding proteins AAG81096 - AAG81241, Mycobacterium tuberculosis proteins which are potential drug targets. The DNA and protein sequences are used to illustrate the method of the invention. The method involves providing an unknown nucleotide or polypeptide sequences, and comparing it to a number of sequences along with at least one algorithm capable of analysing a functional relationship between nucleotide and polypeptide sequences. The method is useful for characterising the function of nucleic acids and polypeptides that may be useful as a target for a drug or essential for the growth or viability of an organism.
                                                                                                                        1529
 24-JUL-2001
                            AAH02079;
                                                      AAH02079
                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identifying nucleotide or polypeptide sequence for use as drug target, involves providing algorithm that analyzes a functional relationship between nucleotide or polypeptide sequences, and comparing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-329193/34.
P-PSDB; AAG81125.
                                                                                                                                                                                                                                            Sequence 3519 BP; 675
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Drug target;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium tuberculosis potential drug target gene SEQ ID 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-SEP-2001
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12-NOV-1999;
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                                                                                                                                                                                       Local Similarity
                                                                                                                                  1 tacggcgtttcgatgaaccc 20
                                                                                                                     TACGCCGTTTCGATGAACCC
                                                      standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              á
                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 68-69;
 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             growth; organism viability; characterisation; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2000US-0179531.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rotstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99US-0165086.
99US-0165124.
                                                     DNA;
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                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                         A; 1081 C; 1183 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                to a method for identifying a nucleotide or
                                                                                                                                                                                                                                                                                                                                                                                                                                                          207pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3519
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Marcotte EM;
                                                      ΒP
                                                                                                                                                                                      Score 20;
Pred. No.
                                                                                                                                                                         Mismatches
                                                                                                                                                                                      0.42;
                                                                                                                                                                                                    DB
                                                                                                                                                                                                                                         580 T; 0 other;
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                                                                                                                                                                                                 Length 3519;
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1 tacggcgtttcgatgaaccc

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1547

20 1528

RESULT

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cc acids of determined algal, archaeal, bacterial, fungal and parasitical consecuency with a combination of defined primer pairs. The method can be used for producing probes and/or primers for detecting one or more created microorganisms e.g. algae, archaea, bacteria, fungi and centerial probes and/or primers for detecting one or more consistency for universal detection and for specific and ubiquitous constants. The method of an algala, archaeal, bacterial, fungi and centerial precise, genus, family and group. A nucleic acid (I) contained using the method of the invention can be used for the universal detection of any bacterium, fungus or parasite in a sample and for the centerion of at least one antimicrobial agent resistance gene or at least one toxin gene. hexa nucleic acids are used for the specific and ubiquitous detection and for identification of Streptococcus pneumoniae. (I) can be used to design a therapeutic agent which is effective against conformation of the design at therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group corynebacterium sp., Enterobacteriaceae group, Escherichia coli, con be used to design at therapeutic agent which is effective against microorganisms. Microbial species or genus or family or phylum or group corynebacteriaceae family, Pseudomonads group, Escherichia coli, coling but a detected include Abiotrophia adiacens, Bordetella sp., colong the specific and coling the series and staphylococcus sp. Using DNA based tests provides faster results than substrate specificity tests as results can be a converted to the colong test and termined.
                          Best
      Matches
                                            Query Match
                                                                                                                                             Neisseria gonorrhoeae and Staphylococcus sp.. Using DNA based tests provides faster results than substrate specificity tests as results can be determined in an hour and improved accuracy is also achieved. AAH00010 to AAH002304 represent nucleotide sequences and primers/probes which are given in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes a method for generating a repertory of nucleic acids of tuf, fus, atpD and/or recA genes from which probes and/or primers are derived. The method comprises amplifying the nucleic acids of determined algal, archaeal, bacterial, fungal and parasitical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Species Species, your indentification; paragraphic identification; algal; archaeal; bacterial; rungal; paragraphic identification; diagnosis; translation elongation factor G; RecA recombinase; resistance; translation elongation factor G; RecA recombinase; antimicrobial;
                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid sequences are used to generate universal probes and primers which can be used to identify and detect the presence of archaeal, bacterial, fungal and parasitical species in a test same
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-SEP-1999;
19-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis nucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-APR-2001
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                        Local
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      20;
                      Similarity
                                                                                                            3534
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MG,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 1478-1479; 1580pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000WO-CA01150
                                                                                                            BP;
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by PH;
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                                                                                                          679 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genus specific;
                      100.0%;
                                                                                                          1081 C;
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                      Score 20;
Pred. No.
  Mismatches
                                                                                                          1188
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                      0.42;
                                                                                                          586
                                          DB 22;
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                                          Length 3534;
                                                                                                          other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  resence of algal,
a test sample -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detection;
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  Gaps
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RESULT 12
AAA89994/c
ID AAA899
XX
AC AAA899
XT 18-DEC
XX
DT 18-DEC
XX
KW Drug r
KW Drug r
KW RNA PO
XX
OS Mycoba
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ID AAA746
XX
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                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the rpoB gene from Mycobacterium tuberculosis. Rifampin resistance is largely associated with point mutations localised in a small core region of 81 base pairs in the rpoB gene, which encodes the RNA polymerase beta subunit. To detect a mutation, a complex is formed comprising a first sequence representing the predetermined region of the gene of the organism and a second sequence representing the corresponding region of the gene of the wild type organism in double stranded form. Each member of at least one pair of non-complementary trands within the complex has a label. The association of the labels in the complex is related to the presence of the mutation. The presence of
                                                                                                          18-DEC-2000
                                                                                                                                     AAA89994;
                                                                                                                                                             AAA89994 standard;
                                                                                                                                                                                                                                2122 TACGGCGTTTCGATGAACCC 2103
                                                                                                                                                                                                                                                                                                                                                      Sequence 3853 BP; 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        particularly
tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Method for detecting drug resistance in a strain of an organism particularly for detecting rifampin resistance in Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-524243/47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mycobacterium tuberculosis; rpoB; RNA polymerase beta subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAA74651 standard;
                                                     Drug resistance;
                                                                                M. tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (DADE-) DADE BEHRING INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rifampin resistance; mutation detection; ds.
               Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                    Local Similarity hes 20; Conserv
                                                                                                                                                                                                                                                1 tacggcgtttcgatgaaccc 20
                                        polymerase beta subunit;
                                                                                                                                                                                                                                                                                                                                                                                mutation is related to the drug resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kurn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fig 4; 86pp; English.
                                                                                                                                                                                                                                                                                      Conservative
                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tuberculosis rpoB gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99WO-US30377.
                                                                             rpoB gene encoding RNA polymerase beta subunit.
                                                    rifampin; rifampicin;
                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                                 100.0%;
                                                                                                                                                                                                                                                                                                                                                      A; 1173 C; 1293 G;
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                                          as.
                                                                                                                                                                                                                                                                                                 Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                       Mismatches
                                                    pyrazinamide;
                                                                                                                                                                                                                                                                                                  0.42;
                                                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                      664 T;
                                                                                                                                                                                                                                                                                                              21;
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                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                 of the strain.
                                                                                                                                                                                                                                                                                                            Length 3853;
                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                      other;
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AAT12096
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention relates to a method for detecting drug resistance in a strain of an organism. The method comprises detecting the presence of a least 1 mutation in a first sequence and relating the presence of the mutation to drug resistance. Included in the invention are a kit for carrying out the method and a method for detecting the presence of a difference between two related nucleic acid sequences in an organism. I methods are useful for detecting resistance to drugs such rifampin and pyrazinamide in Mycobacterium. The present sequence represents the Mycobacterium tuberculosis rpoB gene (which encodes the RNA polymerase beta subunit). The sequence is used in an example of the method of the invention for the detection of rifampin resistance in M. tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Detecting resistance of drugs such as rifampicin in strains {\tt Mycobacterium}, comprising detecting mutations in a gene and them to drug resistance -
                                                                        09-JUN-1995;
                                                                                                                                                                                                 determination;
                                                                                                                                                                                                             Antibiotic; resistance; spectrum; gene; mycobacterium;
                                                                                                                                                                                                                                                                                                                                                                                 2122 TACGGCGTTTCGATGAACCC
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22-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-DEC-1999;
                      (INNO-) INNOGENETICS NV.
                                                                                                14-DEC-1995.
                                                                                                                         WO9533851-A2
                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                        M. tuberculosis rpoB gene fragment amplification
                                                                                                                                                                                                                                                                  10-JUL-1996
                                                                                                                                                                                                                                                                                                                   AAT12096 standard; DNA; 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3853 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Fig 4; 91pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-499235/44
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                                                                                                                                                                                                                                                                                                                                                                                                        1 tacggcgtttcgatgaaccc
                                                                                                                                                                          differential; hybridisation; pattern;
in; species identification; ss.
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                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                   amplification;
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99US-0296894
                                               94EP-0870093
                                                                        95WO-EP02230
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                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
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Pred. No. 0.42;
                                                                                                                                                                                                   tuberculosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              G; 664 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
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                                                                                                                                                                                                                                        primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              other;
                                                                                                                                                                                                   tragment;
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relating
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De Beenhouwer H,

Jannes G,

Machtelinckx L,

Portaels

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RESULT 14
AAQ51532/c
ID AAQ515
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Best Local S
Matches 19
                                                                 17-SEP-1992;
30-APR-1992;
14-AUG-1992;
16-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The antibiotic resistance spectrum (ARS) of a mycobacterium can be determined by amplifying the relevant part of the antibiotic resistance gene, i.e. the M. tuberculosis rpoB gene fragment amplified using the primer set ART12091-98, hybridising it with a least 1 rpoB gene probe, detecting the hybrids formed and inferring the ARS, and opt. the spp., from the differential hybridisation patterns. The method is partic. useful for the detection of rifampicin and/or rifabutin resistance in M. leprae or M. tuberculosis, and mycobacterial spp. identification. The method is rapid and reliable and provides simultaneous determn.
 (ASSI-)
(INSP)
(MEDI-)
(UYBE-)
(UYPA-)
                                                                                                                        30-APR-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Probes and primers for determn. of antibiotic resistance spectrum of Mycobacterium, opt. coupled with species identification - from different patterns of hybridisation with rpoB gene
                                                                                                                                             11-NOV-1993
                                                                                                                                                                                                                                                                                                             rifampicin;
                                                                                                                                                                                                                                                                                                                                    M.leprae
                                                                                                                                                                   W09322454-A
                                                                                                                                                                                                                                                                              Mycobacterium
                                                                                                                                                                                                                                                                                                                                                          17-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                     AAQ51532 standard; DNA; 3447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and spp. identity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      . Similarity
19; Conser
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AIND
                       MEDICAL RES COUNCIL.
                                ASSISTANCE PUBLIQUE INST PASTEUR.
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                                                                                                                                                                                                                                                                                                              antibiotic;
BERNE.
CURIE PARIS VI P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                          (first
                                                                                                                                                                                                                                                                              leprae.
                                                                 92FR-0011098.
92US-0875940.
92US-0929206.
93FR-0004545.
                                                                                                                                                                                                                                                                                                                                    gene
                                                                                                                       93WO-EP01063
                                                                                                                                                                         /*tag= a
/note= "rifampicin-sensitive; in resistant
strains the Ser codon (TCG at
nucleotides 1273-1275) is often mutated
to a Phe, Met or esp. Leu codon"
                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.0%;
                                                                                                                                                                                                                                                                                                             susceptibility; sensitive;
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Yamamoto F
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27-NOV-2000;
22-DEC-2000;
16-FEB-2001;
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23-MAY-2000;
26-MAY-2000;
                New polynucleotides antibiotics, compris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence of the rpoB gene from sensitive strains (AAQ51532) revealed mutations in the region encoding amino acids 400-450. A common mutation seen in resistant strains occurs at codon 425 where Ser is substituted, most frequently by Leu.
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resistant Mycobacterium leprae strains. A comparison with the
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2000US-206848P.
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The invention relates to antisense inhibitors of genes essential to CC prokaryotic cellular proliferation, their use in identifying the CC genes, their use in the discovery of novel antiblotics, the essential CC genes themselves and the encoded proteins. The prokaryotes used are Escherichia coli, Staphylococcus aureus, Salmonella typhi, Klebsiella CC pneumoniae, Pseudomonas aeruginosa and Enterococcus faecalis. The CC invention is also useful for the identification of potential new targets CC for antibiotic development. The antisense nucleic acids can also be used to identify proteins used in proliferation, to express these proteins. CC and to obtain antibodies capable of binding to the expressed proteins. CC The proteins can be used to screen compounds in rational drug discovery CC programmes. The antisense nucleic acid sequence is also useful to screen CC for homologous nucleic acids which are required for cell proliferation in CC awide variety of organisms. The present sequence encodes an CC essential prokaryotic cellular proliferation protein. CC Note: The sequence data for this patent did not form part CC format directly from WIPO at CC format directly from WIPO at
                                                                                                                                                                  Query Match 84.0%; Score 16.8; I Best Local Similarity 90.0%; Pred. No. 21; Matches 18; Conservative 0; Mismatches
1 tacggcgtttcgatgaaccc 20
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1652 TAAGGCGTTTCGATGAAACC 1633
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/strain="H37"	/organism="Mycobacterium tuberculosis"	1432	Location/Qualifiers	Antimicrob. Agents Chemother. 341, 647-650 (1993)	tuberculosis	Detection of rifampicin-resistance mutation in Mycobacterium	Colston, J., Matter, L., Schopfer, K. and Bodmer, T.	Telenti, A., Imboden, P., Marchesi, F., Lowrie, D., Cole, S.T.,	1 (bases 1 to 432)	Mycobacterium; Mycobacterium tuberculosis complex.	Actinomycetales; Corynebacterineae; Mycobacteriaceae;	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;	Mycobacterium tuberculosis	Mycobacterium tuberculosis (strain H37) DNA.	RNA polymerase beta-subunit; rifampicin resistance.	L05910.1 GI:149991	L05910	resistance gene, complete cds.	Mycobacterium tuberculosis RNA polymerase beta subunit; rifampicin	MSGRIFRNAP 432 bp DNA linear BCT 21-MAY-1993		

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/protein_id="AAB59068.1"
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Unknown.
Unclassified.
1 (bases 1 to 620)
Kaiser.M.W., Lyamichev,V.I. and Lyamichev,N.
Cleavage of nucleic acid acid using thermost
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1 (bases 1 to 620)

1 (bases 1, Lyamichev, V.I. and Lyamichev, N.

Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.

Cleavage of nucleic acid acid using thermostable methoanococcus jannaschii FEN-1 endonucleases
Patent: US 5843669-A 135 01-DEC-1998;
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Sequence 136 from patent US 5843669.
AR062057
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20; Conserv
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AR062056
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Heym,B., Cole,S., Young,D.,
Bodmer,T.
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AR062058
                                                                                 l (bases 1 to 620)

Kaiser M.W., Lyamichev, V.I. and Lyamichev, N.

Cleavage of nucleic acid acid using thermostable

Jannaschii FEN-1 endonucleases

Patent: US 5843669-A 138 01-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                              Unclassified.

( bases 1 to 620)

Kaiser, M.W., Lyamichev, V.I. and Lyamichev, N.

Cleavage of nucleic acid acid using thermostable jannaschii FEN-1 endonucleases

Patent: US 5843669-A 137 01-DEC-1998;
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Patent: US 5843669-A 136 01-DEC-1998;
Location/Qualifiers
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Sequence 138 from patent
AR062059
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Raiser M.W., Lyamichev, V.I. and Lyamichev, N.

Cleavage of nucleic acid acid using thermostable methoanococcus

jannaschii FEN-1 endonucleases

Patent: US 5843669-A 139 01-DEC-1998;

Location/Qualifiers

1. 620
 AF060353 705 bp
Mycobacterium tuberculosis RNA
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Sequence 140 from patent
AR062061
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                                                                                                                                                                                                             AR149128
Sequence 24
AR149128
AR149128.1
                                                Unclassified.

1 (bases 1 to 706)
Gingeras T.R., Mack,D., Chee,M.S., Ber Ghandour,G. and Wang,C.
Chip-based species identification and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drobniewski,F., Gnandour,G., Wang,E., Berno,A., Small,P. Drobniewski,F., Alland,D., Desmond,E., Holodniy,M. and Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.
1 (bases 1 to 705)
              of microorganisms
Patent: US 6228575-A 24 08-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (20-APR-1998) Division of Infectious Disease, Affymetrix, 3380 Central Expressway, Santa Clara, CA 95051, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genome Res. 8 (5), 435-448 (1998) 98248685
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227 c 250
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/protein_id-"AAC38533.1"
/protein_id-"AAC38533.1"
/db_xref="GT:3313465"
/translation-"QDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
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FGFTETPYKRVDGYVSDEITYYLTMADEEDRHYVAAAKSFIDAADGRFYEPFATUVRRKAB
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/db_xref="taxon:1773"
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/strain="ATCC27294"
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150706
150706.1
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Detection of a genetic locus encoding resistance mycobacterial cultures and in clinical specimens Patent: US 5643723-A 1 01-JUL-1997; Location/Qualifiers
                                                                                   Highly conserved genes and their use to for detection of microorganisms Patent: Wo 0123604-A 2072 05-APR-2001; Infectio Diagnostic (I.D.I.) INC. (CA)
                                                                                                                                                                                                                                                   Sequence 2072 from Pate
AX111339
AX111339.1 GI:13927631
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                                                                                                                                                                                       Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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/organism="unknown"
227 c 250 g
                                    /organism="Mycobacterium tuberculosis"
/strain="Rv"
                                                                       Location/Qualifiers
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302 c 330 g
             /db_xref="taxon:1773"
1081 c 1188 g
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
gene, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (11-UTL-1994) Paul Imboden, Institute for Medical
Microbiology, University of Berne, Friedbuehlstrasse 51, Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished
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Cole, S., Schopfer, K. and Burkart, T.
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1 (bases 1 to 3853)
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576. .>3853
                                                                                                                                                                 EVEYVPSSEVDYMDVSPROMVSVATAMIPFLEHDDANRALMGANMORQAVPLVRSEAP
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ANQCPIVDAGDRVEAGOVIADGPCTDDGEMALGKNLLVAIHDWEGHDVEDAIIISNRL
VEEDVLTSIHIEEHEIDARDTKLGAEEITRDIPNISDEVLADLDERGIVRIGAEVRDG
                                                                                                                                                                                                                                                      MSRMERVVRERMTTQDVEAITPQTLINIRPVVAAIKEFFGTSQLSQFMDQNNPLSGLT
HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRMCPIETPEGPNIGLIGSLSVYARVNP
FGFIETPYRKVVDGVVSDGIVYLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG
                                                                                                                                                                                                                                                                                                                     TEKGTFIINGTERVVVSQLVRSPGVYFDETIDKSTDKTLHSVKVIPSRGAMLEFDVDK
RDTVGVRIDRKRGPOTVVLLKALGWTSBQIVEREGFSELMRSTLEKDNIYGTDEALLD
IYRKLARGEPDFYKESAOTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEDITSSTL
EEDVVATIEYLVRLHEGQTTMTVPGGVEVPVETDDIDHFGNRRLRTVGELIQNQIRVG
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EDELPAGVNELVRVYVAQKRKISDGDKLAGRHGNKGVIGKILPVEDMPFLADGTPVDI
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                                                                                                    ILNTHGVPRRMNIGQILETHLGWCAHSGWKVDAAKGVPDWAARLPDELLEAQPNAIVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="H37Rv"
/db_xref="taxon:1773"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'gene-"rpoB"
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                    1173
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Miller, L.P., Crawford, J.T. and Shinnick, T.M.
The rpoB gene of Mycobacterium tuberculosis
Antimicrob. Agents Chemother. 38 (4), 805-811 (1994)
94304130
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RNA polymerase beta-subunit; rpoB gene.
Mycobacterium tuberculosis (strain Rv) DNA.
Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20; Conser
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MSRMERVVERMTTQDVBAITPQTLINIRPVVAAIKEFGTSQLSQFMDQNNPLSGLT
MKRRLSALGPGGLSREAGLEVRDVHPSHYGBMCP ETPEGRNIGLIGSLSGVARVNP
FGFIETPYRKVVDGVVSDEIVYLTADEEDRHVVAQANSPIDADGRFVEPRVLVRRKAG
EVEYVPSSEVDYMDVSPROMVSVATAMIPFLEHDDANRALMGANMORQAVPLVRSEAP
LVGTGMELRAAIDAATSSQESGVIE EEVSADYITVMHDUGTRRTYRMRKFARSNHGTC
ANQCPIVDAGDRVEAGQVIADGCCTDDGEMALGKNLLVAIMPMEGHNYEDAIILSNRL
VEEDVLTSIH EEHELDARDTKLGAEELTRDIPNISDEVLADLERGIVRIGAEVRDG
DILVGKVTPKGETELTPEERLLRAIFGEKAREVDTSLKVPHGESGKVIRIGREFARSH
ILVGKVTPKGETELTPEERLLRAIFGEKAREVDTSLKVPHGESGKVIRIGAEVRDG
DILVGKVTPKGETELTPEERLLRAIFGEKAREVDTSLKVPHGESGKVIRIGAEVRDG
DILVGKVTPKGETELTPEERLLRAIFGEKAREVDTSLKVPHGESGKVIRIGAEVRDG
DILVGKVTPKGETELTPEERLLRAIFGEKAREVDTSLKVPHGESGKVIRIGAEVRDG
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DILVGKVTPKGETELTPEERLLRAIFGEKAREVDTSLKVPHGESGKVIRIGAEVRDG
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4641. .>5084
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KLHHLVDDKIHARSTGPYSMITQQPLGGKAQFGGQRFGEMECWAMQAYGAAYTLQELL
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TEKGFTIINGTERVVVSQLVRSJGVYFDETIDKSTSKTIHSVKVIPSRGAWLEEDVDK
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IYRKLRPGEPPTKESAQTLLENLFFKEKRYDLARVGRYKVNKKLGLHVGEPITSSTLT
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/gene="rpoB"
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/transl_table=11
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1065. .4598
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/strain="Rv"
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1065. .4598
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Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., Wille, O., Fleischmann, R.D., Alland, D., Eisen, J.A., Carpenter, L., Wilce, O., Peterson, J., Deboy, R., Dodson, R., Gwinn, M., Ermolaeva, M., Kolonay, J.F., Nelson, W.C., Umayam, L.A., Ermolaeva, M., Kolonay, J.F., Nelson, W.C., Utterback, T., Weidman, J., Khouri, H., Salzberg, S.L., Delcher, A., Utterback, T., Weidman, J., Khouri, H., Salzberg, S.L., and Bishai, W.

Gill, J., Mikula, A. and Bishai, W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fleischmann,R.D., Aliand,D., Eisen,J.A., Carpenter,L., White,O. Peterson,J., DeBoy,R., Dodson,R., Gwinn,M., Haft,D., Hickey,E., Kolonay,J.F., Nelson,W.C., Umayam,L.A., Ernolaeva,M., Salzberg,S.L., Delcher,A., Utterback,T., Weldman,J., Khouri,H., Gill,J., Mikula,A. and Bishai,W.

Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (25-APR-2001) The Institute for Genomic Medical Center Dr. Rockville, MD 20850, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mycobacterium tuberculosis CDC1551.

Mycobacterium tuberculosis CDC1551

Bacteria, Firmicules; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium, Mycobacterium tuberculosis complex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Whole genome comparison of Mycobacterium tuberculosis clinical and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complete genome. AE006964 AE000516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium tuberculosis CDC1551,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ø
                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       163.
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Pred. No. 2.1
0; Mismatches
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gene

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/gene="MT0699"

note="identified

bу

match

to PFAM

protein family HMM

codon_start=1

Glimmer2; putative; conserved authentic frameshift"

is not the result of

note="This region contains an authentic frame shift and

a sequencing artifact; identified

γď

gene

GEQTQNRIAQAFRVRFCVCSPT" complement(8058. .9972)

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CDS

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. 8065)

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CDS

gene

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FLATRLGGQWGGAYGTMPAGLDLAPILERALVKG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="AP endonuclease,
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                                                                                                                                                                                                                                                                          PEGHAFVADAVEHGFRDAVRRRDEPFGDYGRQASRV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="MT0700"
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                                                  Query Match
Best Local :
                                        Matches
1709
          1 tacggcgtttcgatgaaccc 20
TACGGCGTTTCGATGAACCC 1690
                                      ch 100.0%;
l Similarity 100.0%;
20; Conservative 0
                                        0;
                                                 Score 20; DB Pred. No. 2.7;
                                        Mismatches
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                                        0
                                                           Length 19352;
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                                        Gaps
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Search completed: August 7, 2002, 21:51:38 Job time: 23873 sec

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112 113 114 115 116 117 117 118 118 118 118 118 118 118 118	e de	Database :	Minimum DB seq Maximum DB seq Post-processing	Searched: Total number of	Perfect score: Sequence: Scoring table:	OM nucleic - nuc Run on:	
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Sequence 70, Appl Sequence 2, Appli Sequence 6, Appli Sequence 41, Appl Sequence 50, Appl Sequence 59, Appl Sequence 59, Appl Sequence 1, Appli Sequence 1, Appli Sequence 44, Appli Sequence 30, Appl Sequence 9, Appli Sequence 10, Appli Sequence 20, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 16, Appli Sequence 17, Appli Sequence 18, Appli Sequence 18, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli Sequence 31, Appli Sequence 43, Appli Sequence 44, Appli Sequence 45, Appli Sequence 46, Appli Sequence 47, Appli Sequence 47, Appli Sequence 47, Appli Sequence 47, Appli Sequence 47, Appli Sequence 47, Appli	nce to ult be ibutio	* *	,	67066		146.61 Seconds .ignments) .ion cell updates/sec	

Query Match 100.0%; Score 20; DB 4; Length 20; Best Local Similarity 100.0%; Pred. No. 0.23; Matches 20; Conservative 0; Mismatches 0; Indels

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RESULT US-08 US-08 Seque Pates GENNA ANA ANA ANA ANA ANA ANA ANA ANA ANA	
SSULT 1 S-08-750-088A- Sequence 70, Patent No. 63 GENERAL INFO APPLICANT: COUNTRY: COUNTRY: COMPUTER R MEDIUM T COMPUTER R APPLICAT COMPUTER R APPLICAT ATTORNEY/A NAME: CURRENT ARE APPLICAT TOPELOMUND TELEPAN: INFORMATION SEQUENCE C LENGTH: TYPE: TYP	544371109887658433711098
T 1 -750-088A-70 uence 70, Appl ent No. 632913 NERAL INFORMAT APPLICANT: MA APPLICANT: D.C. COUNTRY: USSTREET: 10.C. COUNTRY: USSTREET: D.C. COUNTRY: USSTREET: USSTREET: CALSSIFICATION FILLING DATE: CLASSIFICATION REFERENCE/DO TELECOMMUNICAT TELEPANUE: TELEFAX: 20 FORMATION FOR SEQUENCE CHARA SEQUENCE TYPE: MOLECUE TY	
IN LOCAL DEPTH OF THE CONTROL OF THE	777777777777777777777777777777777777777
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US/08750 WER, HAN FRAN OIS KX, LIEV ERT DI TI TI KESSISTANC TAR C-DOS/MS C-DOS/MS C-DOS/MS TION: REBER AVENU TION: RGE A. 1-1997	44444444444
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OF THE OF MYCOB	7-935A-8 7-935A-12 7-935A-12 7-935A-13 7-935A-17 7-935A-19 7-935A-21 7-935A-24 7-935A-24 7-935A-24 7-935A-30
ANTIBIOTIC ACTERIUM SPECIES	Sequence 8, A Sequence 12, Sequence 14, Sequence 17, Sequence 17, Sequence 19, Sequence 21, Sequence 21, Sequence 22, Sequence 23, Sequence 29, Sequence 30, Sequence 32, Sequence 34, Sequence 35, Sequence 35, Sequence 36, Sequence 36, Sequence 36, Sequence 38,
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RESULT 4
US-09-147-935A-7
; Sequence 7, Application US/09147935A
; Patent No. 6242584
                                                                                                                                                                                                                                                                                                 ; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 6
; LENGTH: 306
; TYPE: DNA
; ORCANISM: Mycobacterium bovis
US-09-147-935A-6
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; TYPE: DNA
; ORGANISM: MYCObacterium africanum
US-09-147-935A-2
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Matches 20
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Best Local Similarity
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CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEC ID NOS: 50
SOFTWARE: KOPATIN 1.0
SEC ID NO 2
SEC ID NO 2
                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KOK, YOON-HOH
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF POB GENE
TILE REFERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR APPLICATION NUMBER: DS/07-28
NUMBER OF SEQ ID NOS: 50
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APPLICANT: KIM, Bum-JOON
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF TPOB GENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 0136/0F425
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100.0%; Pred. No. 0.24;
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RESULT 6
US-09-147-935A-50
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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-41
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                                                                                                  Sequence 50, Application US/09147935A
Patent NO. 6245384
GENERAL INFORMATION:
APPLICANT: KOOK, Yoon-Hoh
APPLICANT: KIM, Bum-Joon
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SEQ ID NO 41
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Best Local Similarity
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SEQ ID NO 7
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CURRENT APPLICATION NUMBER: US/09/147,935A CURRENT FILING DATE: 1999-03-19 PRIOR APPLICATION NUMBER: PCT/KR98/00228
                                              TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF TOOB GENE FILE REFERENCE: 0136/0F425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF TOOB GENE FILE REFERENCE: 0136/07425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILLING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR FILING DATE: 1998-07-28
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APPLICANT: KOOK, Bum-Joon
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rPOB GENE
FILE REFERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR FILING DATE: 1998-07-28
NUMBER OF SEQ ID NOS: 50
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TYPE: DNA
ORGANISM: Mycobacterium bovis
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; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
US-09-147-935A-50
                                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic) US-08-313-185-59
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Matches 20
                             Query Match 100.
Best Local Similarity 100.
Matches 20; Conservative
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SEQ ID NO 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Heym, Beate
APPLICANT: Cole, Stewart
APPLICANT: Young, Dougla:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR FILING DATE: 1
NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                       TELEFAX: (202) 408-4400 INFORMATION FOR SEQ ID NO: 59:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: APPLICANT:
                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 25, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/0 FILING DATE: 12-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Finnegan, Henderson, Farabow, Garrett ADDRESSEE: Dunner
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Zhang, Ying
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                                               100.0%;
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Pred. No. 0.2
0; Mismatches
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RESULT 9
US-08-250-030-1
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; MOLECULE TYPE:
US-09-082-614A-59
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                                                                     Sequence 1, Application US/08250030 Patent No. 5643723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 59, Application US/09082614A Patent No. 6124098
                                                                                                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                  Matches
GENERAL INFORMATION:
APPLICANT: Persing,
TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08
FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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ADDRESSEE: Dunner
ADDRESSEE: Dunner
ADDRESSEE: N.W.
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APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (202) 408-4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                               18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 02356.0068-00000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Meyers, Kenneth REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18
                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                          single
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David H.

Detection of a Genetic Locus Encoding
Resistance to Rifampin in Mycobacterial Cultures and in
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                                                                                                                                                                                                                                                                 Score 20;
Pred No.
                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                   0.25;
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                                                                                                                                                                                                                                                                                  Length 432;
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TITLE OF INVENTION: C1
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:

Clinical Specimens

STREET:

ADDRESSEE:

E: Schwegman, Lundberg & Woessner 3500 IDS Center

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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1, Application PC/TUS9506790 GENERAL INFORMATION:
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Best Local (
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/06790
FILING DATE: 26-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 150
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: RABSCh, Kevin W.
REGISTRATION NUMBER: 35,651
REFERENCE/DOCKET NUMBER: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: Mueting, Ann M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Mayo Foundation for Medical Education and Research
APPLICANT: and Hoffmann-La Roche Inc.
TITLE OF INVENTION: Detection of a Genetic Locus Encoding
TITLE OF INVENTION: Resistance to Rifampin
                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261 TACGGTCGGCGAGCTGATCC 280
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FILING DATE: 26-MAN
CLASSIFICATION: 43
                                                                      FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                      COUNTRY: UZIP: 55402
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llarity 100.0%;
Conservative (
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   150.105WO1
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Pred. No. 0.25;
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Best Local Similarity
Matches 19; Conserva
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US-08-750-088A-30
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                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 44
LENGTH: 306
TYPE: DNA
ORGANISM: Mycobacterium xenopi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                        Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: KOOK, YOON-HOH
APPLICANT: KIM, Bum-JOON
TITLE OF INVENTION: A WETHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES BY
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF IPOB GENE
FILE REFERENCE: 0136/0F425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/147,935A CURRENT FILING DATE: 1999-03-19 PRIOR APPLICATION NUMBER: PCT/KR98/00228 PRIOR FILING DATE: 1998-07-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 612-339-3061 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                        GENERAL INFORMATION:
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE:
                                                                                                                                        APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 970 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 11
MOLECULE TYPE:
                                                                         NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                        APPLICANT: ROSSAU, RUDI
TITLE OF INVENTION: MET
TITLE OF INVENTION: RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   261 TACGGTCGGCGAGCTGATCC 280
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS: single
                            CITY: WASHINGTON
                                           STREET:
COUNTRY:
                                                          ADDRESSEE:
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5. 6329138
             D.C.
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                                           E: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C. 1100 NEW YORK AVENUE, SUITE 600
                                                                                                                                                                      MACHTELINCKX, LIEVE
                                                                                                                                                       JANNES, GEERT
                                                                                                                                                                                       DE BEENHOUWER, HANS
PORTAELS, FRAN OISE
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                                                                                         METHOD FOR DETECTION OF THE ANTIBIOTIC RESISTANCE SPECTRUM OF MYCOBACTERIUM SPECIES 71
                                                                                                                                                                                                                                                                                                                                                                                                                 95.0%;
100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                 Score 19;
Pred. No.
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0.75;
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; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: KOPATIN 1.0
; SEQ ID NO 4
; LENGTH: 306
; TYPE: DNA
; ORGANISM: Mycobacterium aurum
US-09-147-935A-4
RESULT 14
US-09-147-935A-9
US-09-147-935A-9
; Sequence 9, Application US/09147935A
; Patent No. 6242584
; GENERAL INFORMATION:
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US-09-147-935A-4
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; MOLECULE TYPE:
US-08-750-088A-30
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NAME: GOLDSTEIN, JORGE A.
REGISTRATION NUMBER: 29,021
REFERENCE/DOCKET NUMBER: 1657.0010000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2540
TELEPHONE: 202-371-2540
INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENCTH: 25 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09147935A

Patent No. 6242584

GENERAL INFORMATION:
APPLICANT: KOK, Yoon-Hoh
APPLICANT: KIM, Bum-Joon
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF rPOB GENE
FILE REFERENCE: 0136/0F425
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR FILING DATE: 1998-07-28
NUMBER DE SEC IT NOC: 50
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Best Local Similarity 95.0%;
Matches 19; Conservative
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Best Local Similarity
Matches 19; Conserv
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/750,088A
FILING DATE: 21-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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SEQ ID NO 9
LENGTH: 306
TYPE: DNA
ORGANISM: Mycobacterium celatum Type2
US-09-147-935A-9
Search completed: August Job time: 24011 sec
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                                                                                                                                                                                                                                           SOFTWARE: KOPATIN 1.0
SEQ ID NO 10
LENGTH: 306
TYPE: DNA
ORGANISM: Mycobacterium chelonae
US-09-147-935A-10
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US-09-147-935A-10
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                                                                                                                                             Query Match
Best Local Similarity 95.0
Matches 19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 10, Application US/09147935A Patent No. 6242584
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Best Local Similarity
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CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR FILING DATE: 1998-07-28
NUMBER: OF SEQ ID NOS: 50
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                              APPLICANT: KOOK, YOON-HOH
APPLICANT: KIM, BUMT-JOON
TITLE OF INVENTION: A METHOD FOR IDENTIFYING MYCOBACTERIAL SPECIES
TITLE OF INVENTION: COMPARATIVE SEQUENCE ANALYSIS OF TPOB GENE
FILE REFERENCE: 0136/0F425
CURRENT APPLICATION NUMBER: US/09/147,935A
CURRENT FILING DATE: 1999-03-19
PRIOR APPLICATION NUMBER: PCT/KR98/00228
PRIOR FILING DATE: 1998-07-28
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Perfect score:
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Copyright (c) 1993 - 2000 Compugen
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BE4448100

BE444713

BE195103
  BE442518
BG299722
BI188703
BI981973
BI888442
AW502654
AW501791
BE101908
AW502300
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BM397871 5009-0-38
BM398055 5009-0-42
BM398255 5009-0-42
AL143232 Anopheles
BE445100 WHE1132_B
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B1888442 ZF637-2-0
AW501791 UI-HF-BR0
AW501791 UI-HF-BR0
BE101908 UI-R-BO1-AW502300 UI-HF-BR0
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UD422107 13 GHG OF	BG4/3029 002320333	DATE OF COURTS	B1911230 603062995	BI544719 603242678		AZ359615 1M0102G02	BB316372 BB316372	AL508804 AL508804	BH402082 AG-ND-156	AZ178000 SP_0149_A	BG411877 OV2_39_C0	BM318224 PI1_79_A0	യ	8 HV_CEE		C72862 C72862 Rice	_	BG263401 WHE2341_E	BG412215 OV2_39_C0	BE419003 WWR020.D1	BM318366 PI1_77_G0			BM320891 rockefell	BM321334 rockefell	BM320964 rockefell	BM321268 rockefell	AW502130 UI-HF-BR0

ALIGNMENTS

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RESULT 1
BM397871/c
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AUTHORS
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Query Match
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Eukaryota; Alveolata; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 130)
Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frankel,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain CU428.1, growing cells Unpublished (2002)
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BM397871
                                                                                                                                                                                                                                                                                                                                                                                              University of Chicago
920 E. 58th Street, Chicago, IL 60637,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST.
                                                                                                                                                                                                                                                                                                               Email: apturkew@midway.uchicago.edu
Seq primer: T3.
                                                                                                                                                                                                                                                                                                                                                             Tel: 773 702 4374 Fax: 773 702 3172
                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecular Genetics and Cell Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Turkewitz AP
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                                                                                                  /db_xref="taxon:5911"
/clone_lib="chilcoat/Turkewitz cDNA (large fraction)"
/clone_lib="chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
proc. Natl. Acad. Sci USA, 98: 8709-8713."

41 c 44 g 18 t 1 others
                                                                                                                                                                                                                               /organism="Tetrahymena thermophila"
/strain="CU428.1"
                                                                                                                                                                                                                                                                                             location/Qualifiers
92.0%;
95.0%;
Score 18.4; DB 10; Pred. No. 1.7e+02;
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                   Length 130;
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BM396091/c
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                            ,J. and Klobutcher,L.
EST from Tetrahymena thermophila, strain
Unpublished (2002)
                                                                                                  Tetrahymena thermophila.
Tetrahymena thermophila
Tetrahymena thermophila
Eukaryota; Alveolatta; Ciliophora; Oligohymenophorea;
Hymenostomatida; Tetrahymenina; Tetrahymena.
                                                                                                                                                                                                        BM398255 134 bp mRNA linear EST 17 5009-0-42-H08.t.l Chilcoat/Turkewitz cDNA (large fraction) Tetrahymena thermophila cDNA, mRNA sequence.
                 Contact: Turkewitz AP
                                                                        1 (bases 1 to 134)
Turkewitz,A.P., Karrer,K.M., Jahn,C.,
                                                                                                                                                                                 ВМ398255.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Molecular Genetics and Cell Biology University of Chicago 920 E. 58th Street, Chicago, IL 606 Tel: 773 702 4374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2002)
Contact: Turkewitz AP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Turkewitz,A.P., Karrer,K.M., Jahn,C., Orias,E., Kirk,K.E., Frani
,J. and Klobutcher,L.
,J. Trom Tetrahymena thermophila, strain CU428.1, growing cells
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BM396091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: apturkew@midway.uchicago.edu
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/strain="CU428:1"
/db_xref="Texxon:5911"
/clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
Proc. Natl. Acad. Sci USA, 98: 8709-8713."
a 42 c 44 g 19 t
   Genetics
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1. .132
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and Cell Biology
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Pred. No. 1.7e+02;
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                                                                        Kirk, K.E.,
                                           growing
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            l Similarity
18; Conserv
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              Conservative
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1 tacggtcggcgagctgatcc 20
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                                                                                                                                                                                                                                                                                                         2 (bases 1 to 984)
Roth,C.W., Brey,P.T., Ke,Z., Collins,F.H. and Direct Submission
Submitted (16-FEB-2000) BBMI, Institut Pasteur
                                                                                                                                                                                                                         Roux, Paris 75015, France
This clone is from an A. gambiae BAC library provided by F.H. Collins and sequenced by Genoscope in collaboration with the Laboratory of Biochem. and Biol. Molec. of Insects, Institut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CNS01GJZ 984 bp DNA linear GSS 01-JUN-2001 Anopheles gambiae GSS T7 end of clone 06016 of NotreDame1 library from strain PEST of Anopheles gambiae (African malaria mosquito),
                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-FEB-2000) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic survey sequence.
AL143232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     University of Chicago
920 E. 58th Street, Chicago,
Tel: 773 702 4374
Fax: 773 702 3172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Anopheles gambiae
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19; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: apturkew@midway.uchicago
                                                                                                                                                                                                                                                                                                                                                                                      Web : www.genoscope.cns.fr) (bases 1 to 984)
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    272
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/db_xref="taxon:7165"
/clone="06016"
/clone=lib="NotreDame1"
/note="end : T7"
a 236 c 241 g 23:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Chilcoat/Turkewitz cDNA (large fraction)"
/note="Vector: BlueScript2 SK+; Details on library
preparation can be found in Chilcoat and Turkewitz (2001)
proc. Natl. Acad. Sci USA, 98: 8709-8713."
44 c 46 g 18 t
                                                                                                              /organism="Anopheles gambiae"
/strain="PEST"
                                                                                                                                                                                  Location/Qualifiers
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/strain="CU428.1"
/db_xref="taxon:5911"
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95.0%;
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Pred. No. 1.7e+02;
0; Mismatches 1;
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87.0%; 94.7%;

Score 17.4; Pred. No. 7

.4e+02; DB 12;

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984; 0

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ggtcggcgagctgatcc 20
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Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat
                                                                           l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 5105595818
Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                genomes - Normalized root cDNA library Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Triticum aestivum
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                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="Five day old etiolated seedling"
/lab_host="E. coli DH10B"
/note="Vector: Lambda Uni ZAP XR, excised phagemid
/note="Vector: Lambda Uni ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
                                                                                                                                                                                                                                                excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyer lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                    California, Riverside. excised to give pBlue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE1122_B06_C12"
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Matches Query Match Best Local

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Score 17; Pred. No. Mismatches

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BE445100
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(bases 1 to 544)

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.

The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library
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Seq primer: Stratagene SK primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2000)
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oandersn@pw.usda.gov
                                                 California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of phagemid library and normalization were done in HT Nguyer lab by D. Zhang at Texas Tech University. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                     dishes. Roots were harvested. The tissue, total RNA, poly(A) RNA were prepared, a cDNA library was made i TJ Close lab (Choi, Close, Fenton) at the University
                                                                                                                                                                                                                                                                                                                                 pBluescript SK; Site_1: EcoRI; Site_2: Xhoī; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization
                                                                                                                                                                                                                                                                                                                                                                                                                                        /tissue_type="Root"
/tissue_type="Root"
/dev_stage="Five day old etiolated seedling"
--- hact="E. coli DH10B"
--- hact="E. coli DH10B"
                Anderson lab (all other authors).
173 c 132 g 118 t
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/clone="num:"...
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/cultivar="Chinese Spring"
                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="Vector: Lambda Uni-ZAP XR, excised phagemid
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1 (bases 1 to 558)
Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han P.S., Hsda,C.C., Kang,Y., Lazo,G.R., Miller,R., Nguyen,H.T., Rausch,C.J., Seaton,C.L., Tong,J.C. and Zhang,D.
The structure and function of the expressed portion of the wheat
                                                                                                                                                                                l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence have been trimmed to remove vector sequence and quality sequence with phred score less than 20 Seq primer: Stratagene SK primer. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research
US Department of Agriculture, Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595818
Fax: 5105595818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: oandersn@pw.usda.gov
                                                                                                                                                                                                                                                                                                                                        122
                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note-"Vector: Lambda Uni-ZAP XR, excised phagemid /note-"Vector: Kambda Uni-ZAP XR, excised phagemid pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were surface-sterilized, germinated and grown aseptically in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Roots were harvested. The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. The cDNA clones were in vivo excised to give pBluescript phagemids before normalization was carried out. The mass excision of normalization was carried out.
                                                                                                                                                                                                                                                                                                                                     phagemid library and normalization were done in HT Nguyen lab by D. Zhang at Texas Tech Univeristy. Normalization protocol used was that of Soares. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
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/db_xref="taxon:4565"
/clone="WHE1137_H03_005"
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/lab_host="E. coli DH10B"
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                                                                                                                                                                                                     Score 17; DB 10;
Pred. No. 9.8e+02;
                                                                                                                                                                                  Mismatches
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HVSMEh0088E21f Hordeum vulgare 5-45 DAP spike EST library
HVCDNA0009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0088E21f,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDNA library Unpublished (2001)
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BE195103
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864 656 4293
l: rwing@clemson.edu
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                                                                                                                                                                                                                                                                                /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; 
Plants were grown in the greenhouse at the University of 
California, Riverside (Fenton, SJ Close, TJ Close), Whole 
spikes with awns trimmed were collected at 5, 10, 15, 20, 
30 and 45 DAP (Fenton). Total RNA was prepared from each 
pool, equal quantities of all six RNA pools were combined, 
poly(A) RNA was purified from the mixture, one primary 
unamplified cDNA library was made, and 1 million pfu were 
in vivo excised to give pBluescript SK(-) cDNA phagemids 
(Choi); In the TJ Close lab at the University of California, 
Riverside. Phagemids were plated and picked at the Clemson 
University Genomics Institute (CUGI) (Begum, Palmer, 
Frisch, Atkins and Wing). Plasmid DNA preparations, DNA 
sequencing and sequence analysis were performed at CUGI 
(Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). 
The sequence has been trimmed to remove vector sequence 
and contains a minimum of 100 bases of phred value 20 or 
above.
http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. http://wheat.pw.usda.gov/gapages/bap/31/cover.html)" 158 g 120 t
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/clone_lib="Hordeum vulgare 5-45 DAP spike EST library
HVcDNA0009 (5 to 45 DAP)"
/tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
                                                                                                                                                                                                                              sequence analysis see
                                                                                                                                                                                                                                                            above. For more details on library preparation and
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/cultivar="Morex"
/db_xref="taxon:4513"
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Best Local Similarity Matches 17; Conserv

Conservative

85.0%; Score 17; DB 9; 100.0%; Pred. No. 1e+03 tive 0; Mismatches

1e+03;

Length 610; Indels

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Query Match

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The structure and function of the expressed portion of the wheat genomes - Normalized root cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: oandersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
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Anderson, O.D., Chao, S.,
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                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                        /dev_stage="Five day old etiolated seedling"
/lab host="E. coll DH10B"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid
pBluescript SK; Site_1: EcoRI; Site_2: XhoI; Seeds were
surface-sterilized, germinated and grown aseptically in
the dark at room temperature on filter paper with water,
nystatin and cefotaxime in covered crystallization
dishes. Roots were harvested. The tissue, total RNA, and
poly(A) RNA were prepared, a cDNA library was made in the
TJ Close lab (Choi, Close, Fenton) at the University of
California, Riverside. The cDNA clones were in vivo
excised to give pBluescript phagemids before
normalization was carried out. The mass excision of
phagemid library and normalization were done in HT Nguyen
lab by D. Zhang at Texas Tech University. Normalization
proparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHEIIOL_HIO_019"
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HVSMEa0021120f Hordeum vulgare seedling shoot EST library
HVCDNA0001 (Cold stress) Hordeum vulgare cDNA clone HVSMEa0021120f.
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,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Oates,R., Choi,D.W.,
, Fenton,R.D. and Main,D.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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Fax: 864 656 4293
Email: rwing@clemson.edu
Total hg bases = 574
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                                                                                                                                                                                                                                                                       /note="vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Seeds were surface sterilized then germinated under axenic conditions in the dark at room temperature on filter paper with water, nystatin and cefotaxime in covered crystallization dishes. Five-day old seedlings were incubated at 5oC for 2 days. Shoots were then harvested, total RNA was prepared, poly(A) RNA was purified, one primary unamplified cDNA library was made, and 600000 pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids. These steps were performed in the TJ Close laboratory at the University of California, Riverside (Choi, Close, Fenton). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations , DNA sequence mass been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or actor in the contains a minimum of 100 bases of phred value 20 or
http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/gpages/bgn/31/cover.html) (http://wheat.pw.usda.gov/gpages/bgn/31/cover.html) 271 c 220 g 165 t
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HVcDNA0001 (Cold stress)"
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                                                                                                                                                                                                                       sequence analysis see
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/db_xref="taxon:4513"
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/lab_host="TJC121"
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18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 73 2.2 gi|7799258|emb|CAB90 (AL355752) putative integral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Chemistry and Biochemistry Advanced Center for Genome Technology, Un 620 Parrington Oval, Norman, OK 73019, US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., M. and Roe,B.
Analysis of a Fusarium sporotrichioides EST database Unpublished (2001)
Other_ESTs: d2e05fs.fl
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI188703 419 bp mRNA linear EST 10 d2e05fs.rl Fusarium sporotrichioides Tri 10 overexpressed library Fusarium sporotrichioides cDNA clone d2e05fs 5', r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 405 325 4912
Fax: 405 325 7762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        membraneprote
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: broe@ou.edu
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                                                                                                                                                                                                                                                           117
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                                                                                                                                                                                                                                                                                                                     /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
cDNA library"
                                                                                                                                                                                                                                                                                                                                                /organism="Fusarium sporotrichioides"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="02e05fs"
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TR:Q9Y4D4
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90.0%;
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100.0%;
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606 bp mRNA linear EST 24-OCT-2001 adult brain Danio rerio cDNA clone 5333151 5' Q9Y4D4 KIAAO648 PROTEIN ;, mRNA sequence.
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Pred. No. 1.1e
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1.1e+03;
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18; Conser
 Eukaryota;
               Danio rerio
                               zebrafish.
                                                           BI888442.1
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                                                                                      mRNA sequence.
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                                                                                                                                                                     BI888442
ZF637-2-000197 Zebrafish shield
MPMGp637 Danio rerio cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I Tel: 314 286 1800
Fax: 314 286 1810
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Clark, M., Johnson, S.L., Lehrach, H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        High quality sequence stop: 446.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Missouri (web address: www.genomesystems.com) (email contact: info@genomesystems.com) and Research Genetics, Huntsville, Alabama (web address: www.resgen.com) (email contact: info@resgen.com) and RessourcenZentrumPrimarDatenbank, Berlin, Germany (web address:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA Library Preparation: John Ngai. cDNA Library Arrayed Matthew Clark. DNA Sequencing by: Washington University Ge Sequencing Center Clone distribution: Genome Systems, St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1998)
Other_ESTs: fu53f08.x1
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BI981973.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WashU Zebrafish EST Project 1998
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Actinopterygii; Neopterygii; Teleostei;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cyprinidae; Danio.
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library."
133 c 139 g 125 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="adult"
/lab_host="E. coli DH10B"
/note="Vector: pZIPLOX; Site_1: Not1; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="zebrafish adult brain"
/sex="mixed male and female"
/tissue_type="brain"
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/db_xref="taxon:7955"
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Metazoa; Chordata;
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Pred. No. 1.2e
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  Craniata;
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  Vertebrata; Euteleostomi;
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Ostariophysi; Cypriniformes
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                                                                            Email: cgapbs-r@mail.nih.gov
Eco RI site shown at the beginning of the sequence.
Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: M.B. Soares Lab
cDNA Library Arrayed by: M.B. Soares Lab
cDNA Sequencing by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortlum/LLNL at:
                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 292)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW502654 292 bp mRNA 1
UI-HF-BR0p-ajx-b-11-0-UI.r1 NIH_MGC_52 Homo
IMAGE:3075813 5', mRNA sequence.
AW502654
                                                                                                                                                                                                                                               Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
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5' EST sequencing of clones from a zebrafish shield stage library,
normalised from 55,000 starting clones by oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Max-Planck-Institut fuer Molekulare Genetik
Thnestr.63-73, D-14195 Berlin, Germany
Tel: +49 30 8413 1380
Fax: +49 30 8413 1380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Hennig S
laboraty 123, dept.Lehrach
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 640)
Clark, M., Aanstad, P., Hennig, S., Johnson, S.L. and Lehrach, H.
EST sequencing of a zebrafish shield stage cDNA library normalised
by oligonucleotide fingerprinting
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AW502654.1 GI:7117309
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                                        www-bio.llni.gov/bbrp/image/image.html
Seq primer: M13 Forward.
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oligo-dT-Not1 primed, Sal1 adaptors, directionally cloned,
library normalised by oligonucleotide fingerprinting"
a 152 c 139 g 139 t lothers
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/db_xref="taxon:7955"
/clone="MpMGp637_18E17;MPMGp637E1718"
/clone_lib="Zebrafish shield stage whole embryo cDNA
                       Location/Qualifiers
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/tissue_type="whole embryo"
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Pred. No. 1.2e+03;
0; Mismatches 2;
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17; Conserv
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UI-HE-BROp-ajm-g-11-0-UI.rl NIH_MGC_52 Homo IMAGE:3075260 5', mRNA sequence.
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
CDNA Library Preparation: M.B. Soares Lab
CDNA Library Arrayed by: M.B. Soares Lab
DNA Sequencing by: M.B. Soares Lab
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
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/db_xeef="taxon:9606"
/clone=TibAGE:3075260"
/clone_lib="NIH_MGC_52"
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/note="Vector: pT7T3-Pac; Site_1: Not1; Site_2: Eco RI;
/note="Vector: pT7T3-Pac; Site_1: Not1; Site_2: Eco RI;
/constructed from size fractionated cytoplasmic mRNA
(7.4-9.5kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D. "
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/lab_host="DHIOB (LTI)"
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/note="Yector: pT7T3-Pac; Site_1: NotI; Site_1: NotI; Site_1: PT7T3-Pac; 
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/cell_line="MGC85"
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Query Match

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Score 16.4;

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Length 338;

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Best Local Similarity 94.48; Pred. No. 1.6e-03;
Matches 17; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 acggtcggcgagctatc 19
Db 46 ACCOTCCGCCGTCCTCATC 63

Search completed; August 7, 2002, 21:15:17

Job time: 22887 sec
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Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: gb_ba:*
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ALIGNMENTS

ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS REFERENCE AUTHORS RESULT AF057450 LOCUS DEFINITION JOURNAL MEDLINE TITLE PUBMED Mycobacterium afficanum
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bacteria; Firmicutes; Actinobacterineae; Mycobacteriaceae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 306)
Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Bai,G.H., Chae,G.T.,
Kim,B.C., Cha,C.Y. and Kook,Y.H.
Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
99262756 2 (bases 1 to 306) Kook, Y.H., Kim, B.J., AF057450 AF057450.1 GI:5902487 Mycobacterium africanum cds. Mycobacterium africanum. AF057450 10325313 Lee, S.H., Lyu, M.A., Kim, S.J., Bai, G.H., 306 bp DNA linear BCT 17-SEP-1 RNA polymerase beta (rpoB) gene, partial 306 bp BCT 17-SEP-1999

Result

Query Score Match Length DB

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Description

SUMMARIES

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Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)

J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
                                                                                                                                                                                   Submitted (06-APR-1998) Microbiology, College of Medicine, 28 Youngon-dong,
                                                                                                                                                                                                                               Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J., Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
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Mycobacterium bovis RNA
AF057451
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VVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHPSH"
108 g 47 t
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                                           /gene="rpoB"
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                                                                                                                                                      Location/Qualifiers
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<1. .>306
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Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)

J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
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Submitted (06-APR-1998)
College of Medicine, 28
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Kim,S.J., Chae,G.T., Kim,E.J.
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                                                                                                                                                                                                                                                                                                                              /strain="French 1173P2"
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Bai, G.H.,

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Mycobacterium
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Submitted (06-APR-1998) Microbiology,
College of Medicine, 28 Youngon-dong,
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Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)

J. Clin. Microbiol. 37 (6), 1714-1720 (1999)

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            Mycobacterium tuberculosis.

Mycobacterium tuberculosis

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Actinomycetales; Corynebacterineae; Mycobacteriaceae;
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Kook,Y.H., Kim,B.J., Lee,S.H., Lyu,M.A., Kim,S.J.,
Kim,S.J., Chae,G.T., Kim,E.J. and Cha,C.Y.
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Pred. No. 96;
D; Mismatches
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Identification of mycobacterial species by comparative sequence analysis of the RNA polymerase gene (rpoB)
J. Clin. Microbiol. 37 (6), 1714-1720 (1999)
                                                                                                                                                                                                Kook, Y. and Kim, B. Method for identifying mycobacterial sequence analysis of rpoB gene patent: US 6242584-A 2 05-JUN-2001;
                                             20;
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/codon_start=3
/codon_start=3
/trans! table=11
/product="RNA polymerase beta"
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VVAAIKEFFGTSQLSQFMDQNNPLSGLTHKRRLSALGPGGLSRERAGLEVRDVHPSH"

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/strain="H37Rv; ATCC27294"
/db_xref=_ATCC:27294"
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Medicine, 28 Youngon-dong,
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Sequence 6 1
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Rook, Y.-H. and Kim, B.-J.
Method for identifying mycobacterial
sequence analysis of room gene
Patent: US 6242584-A 605-JUN-2001;
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Kook,Y. and Kim,B.

Method for identifying mycobacterial species sequence analysis of rpoB gene patent: US 6242584-A 7 05-JUN-2001;
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                            Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 432)
Telenti, A., Imboden, P., Martchesi, F., Lowrie, D., Cole, S.T., Colston, J., Matter, L., Schopfer, K. and Bodmer, T. Detection of rifampicin-resistance mutation in Mycobacteriu
                                                                                                                                           RNA polymerase beta-subunit; rifampicin Mycobacterium tuberculosis (strain H37) Mycobacterium tuberculosis
                                                                                                                                                                                                                   MSGKIFKNAP 432 bp DNA linear BCT Mycobacterium tuberculosis RNA polymerase beta subunit; resistance gene, complete cds.
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20; Conservative
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Kook, 7. and Kim, B.

Method for identifying mycobacterial species

sequence analysis of rpoB gene

Patent: US 6242584-A 50 05-JUN-2001;
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1 (bases 1 to 306)

Kook, Y. and Kim, B.
Method for identifying mycobacterial species sequence analysis of rpoB gene Patent: US 6242584-A 41 05-JUN-2001;
Antimicrob. Agents Chemother.
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L05910.1 GI:149991
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                                              h 100.0%;
Similarity 100.0%;
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/replace="t"
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/replace="a"
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/replace="c"
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/product="RNA polymerase
/protein_id="AAB59068.1"
/db_xref="GI:149992"
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<1. .>432
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/strain="H37"
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194
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nutation 234 G"
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/replace="ca"
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/replace="t"
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TACGGTCGGCGAGCTGATCC
                                                                                                                                                                                                                                   Unclassified.

1 (bases 1 to 970)
1 (bases 1 to 970)
Persing,D.H., Hunt,J.J., Young,K.K.Y., Felmlee,T./
and Whelan,A.Christian.
Detection of a genetic locus encoding resistance
mycobacterial cultures and in clinical specimens
Patent: US 5643723-A 101-JUL-1997;
Location/Qualifiers
                    AX111339
Sequence 207
AX111339
AX111339.1
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Sequence
150706
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l Similarity 100.0%;
20; Conservative (
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1 (bases 1 to 43;
Heym, B., Cole, S.,
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Sequence 59 from patent US 5851763.
AR067448
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Mycobacterium tuberculosis
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                                        3534 bp
from Patent W00123604
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2 (bases 1 +- 2000)
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Corynebacterineae; Mycobacteriaceae;
Mycobacterium; Mycobacterium tuberculosis complex.

1 (bases 1 to 3853)
Tmbdder b Mycobacterium tuberculosis complex.
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1 (bases 1 to 3534)

Bergeron, M.G., Boissinot, M., Huletsky, A., m Nard, C., Ouellette, M., Picard, F.J. and Roy, P.H.
                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (11-JUL-1994) Paul Imboden, Institute for Medical Microbiology, University of Berne, Friedbuehlstrasse 51, Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U12205.1 GI:515684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MTU12205
3853 bp DNA linear BCT 02-MAR-2000
Mycobacterium tuberculosis H37Rv RNA-polymerase beta subunit (rpoB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Highly conserved genes and their use to for detection of microorganisms Patent: WO 0123604-A 2072 05-APR-2001; Infectio Diagnostic (I.D.I.) INC. (CA)
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MSLSFSDPRFDDVKAPVDECKDKDWTYAAPLFVTAEFINNNTGEIKSQTVFMGDFPMM
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/trans1_table=11
/product="RNA-polymerase beta subunit"
/product="RNA-polymerase beta subunit"
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/db_xref="GI:7144499"
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576. .>3853
TEKGTFIINGTERVVVSQLVRSPGVYFDETIDKSTDKTLHSVKVIPSRGAWLEFDVDK
RDTYGVRIDRKRRQPVTVLLKALGWTSEQIVERFGFSEIMRSTLEKDNTVGTDEALLD
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/strain="Rv"
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EEDVVATIEYLVRLHEGQTTMTVPGGVEVPVETDDIDHFGNRRLRTVGELIONOIRVG
MSRMERVVRERMTTQDVEAITPOTILNIR TRYVAAIKEFFGTSQLSQFMDQNNPLSGLT
HKRRLSALGPGGLSRERAGLEVRDVHPSHYGRMCPIETPEGENIGLIGSLSSLSVA RAVNP
FGFIETFYRKVVDGVVSDGIVYLTADEEDHHVVAQANSPIDADGRFVEBRVLVRRKAG
EVYYPSSEVDYMDVSPRQMVSVATAMIPFLEHDDANRALMGANMORQAVPLVRSEAP
LVGTGMELRAAIDAATSSQOESGVIEEVSADYITVMHDNGTRRTYRMKFARSNHGTC
ANOCPTVDAGDRVEAGQVIADGPCTDDGEMALGKNLLVAIMPWEGHNYEDAIILSNIK
VEEDVLTSIHIEEHEIDARDTKLGAEEITRDIPNISDEVLADLDERGIVRIGAEVRDG
DILVGKVTPKGETELTPEERLLRAIFGEKAREVROTSKKVEHGESGKVIGIRVFSRED
EDELPAGVNELVRYVAAQKRKISDGDKLAGRHGNKGVIGKILPVEDMPFLADGTPVDI
ILNTHGVPRRMNIGQILETHLGWCAHSGWVDDAAKGVPDWAARLPDELLEAQOPNAIVS
TPVFDGAQEAELOGLLSCTLPNBDGDVLVDADGKAMLFDGRSGEPFPYPTVGYMYIM
KLHHLVDDKIHARSTGPYSMITQQPLGGKAQFFGEMECWAMQAYGAAYTLQELL
TIKS"

723 a 1173 c 1293 g 664 t
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Вþ ρy Query Match Best Local Matches 1712 100.0%; Similarity 100.0%; Conservative 0 Score 20; DB Pred. No. 79; Mismatches DB 1; 0; Length 3853; Indels 0; Gaps

0

BASE COUNT ORIGIN

Search completed: August 7, 2002, 21:51:37 Job time: 23872 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

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Perfect score:
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/SIDS1/gcgdata/geneseq/geneseqn-embl/NA1993.DAT:*
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AAA49823
AAA49825
AAX27214
AAX27175
AAX27179
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AAV31045	9968	AAI99683	2	AAS54170	4	AAS02316	AAS59541	σ	AAS99565	AAS99560	AAS99557	AAS99539	AAX27186	AAX27183	AAX27182	AAX27177	AAX27204	AAX27196	AAX27193	AAX27218	AAX27212	AAC88922	AAT12091	AAS59633	AAS99551	AAX27217	AAA89994	AAA74651	AAH02079	AAH51976	AAT09676	AAA49863	6145	995	AAS99530	
Expression vector	Mycobacterium tube	Mycobacterium tube	Drosophila melanog	Pseudomonas aerugi	Drosophila melanog	B. subtilis DNA en	Propionibacterium	Mycobacterium spec	gene	RpoB gene fragment	obacterium tub	M. tuberculosis rp	Propionibacterium	Mycobacterium spec	oB qene fra	+					3	ďΩ	spe	Mycobacterium spec												

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ALIGNMENTS

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Antibiotic; resistance; spectrum; gene; mycobacterium; determination; amplification; tuberculosis; rpoB; fragmen primer; differential; hybridisation; pattern; rifampicin;
         WPI; 1996-040250/04
                          De Beenhouwer H,
Rossau R;
                                                                                        09-JUN-1995;
                                                                                                                                             Synthetic.
                                                                                                                                                                                                         M. tuberculosis rpoB gene fragment amplification primer P2
                                                                                                                                                                                                                           10-JUL-1996
                                                                                                                                                                                                                                             AAT12092;
                                                                                                                                                                                                                                                              AAT12092 standard; DNA;
                                                    (INNO-) INNOGENETICS NV
                                                                       09-JUN-1994;
                                                                                                                                                              rifabutin; species identification; ss.
                                                                                                         14-DEC-1995
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                                                                                                                                                                                                                           (first entry)
                                                                       94EP-0870093
                                                                                        95WO-EP02230
                                  Jannes G,
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Best Local
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      The present sequence is that of the Mycobacterium tuberculosis rpoB (rifampin resistance) gene amplification primer rpoB-F (bp 2201-2220). It is used with the reverse primer given in AAA49824 and with the sequencing primers given in AAA49825 and AAA49826 for the detection and analysis of antibiotic resistance-associated mutations of the rpoB gene (see AAA49863). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and analysis of antibiotic resistance-associated mutations in defined
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The antibiotic resistance spectrum (ARS) of a mycobacterium can be determined by amplifying the relevant part of the antibiotic resistance gene, i.e. the M. tuberculosis rpoB gene fragment amplified using the primer set AAT12091-98, hybridising it with a least 1 rpoB gene probe, detecting the hybrids formed and inferring the ARS, and opt. the spp., from the differential hybridisation patterns. The method is partic. useful for the detection of rifampicin and/or rifabutin resistance in M. leprae or M. tuberculosis, and mycobacterial spp. identification. The method is rapid and reliable and provides simultaneous determn.
                                                                                                                              Claim 4; Page 4; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                         WO200036142-A1
                                                                                                                                                                                                                                                                                                                                                                                   Mycobacterium tuberculosis.
                                                                                                                                                                                                                                                                                                                                                                                                                      Antibiotic resistance; rpoB gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Probes and primers for determn. of antibiotic resistance spectrum of Mycobacterium, opt. coupled with species identification - from different patterns of hybridisation with rpoB gene
    regions of
                                                                                                                                                                                               WPI; 2000-431611/37.
                                                                                                                                                                                                                                                                                                     10-DEC-1999;
                                                                                                                                                                                                                                                                                                                                22-JUN-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA49823 standard;
                                                                                                                                                          tuberculosis
                                                                                                                                                                                                                         Shipman
                                                                                                                                                                                                                                                 (VISI-) VISIBLE GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 20 BP; 3 A; 6 C; 7
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                                                                                                                                                       for the detection and closis with antibiotic
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                                                                                                                                                                    characterization of Mycobacterium
                                                                                                                                                        resistance
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Pred. No.
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(isoniazid),
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                                                                                                                                                                                                                                                                                                                                                                                                                     rifampin resistance; PCR primer;
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0.031;
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                     analysis of antibiotic resistance-associated mutations in def
regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR
(isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), 16S/I
(streptomycin), embB (ethambutol), pncA (pyrazinamide), gyrA
                                                                                                                               rpoB (rifampin resistance) gene sequencing primer rpoB-5s (bp 2201-2220). It is used with the reverse primer given in AAA49826 and with the amplification primers given in AAA49823 and AAA49824 for the detection and analysis of antibotic resistance-associated mutations of the rpoB gene (see AAA49863). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and
                                                                                                                                                                                                                                                                                                                                                                                  Claim 4; Page 5; 43pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for the detection and characteriz tuberculosis with antibiotic resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (streptomycin), embB (etnambulou), pure (grandless), (ciprofloxacin) and 23S (azithromycin) genes (the detection and These primers can be used in a method for the detection and These primers can be used in a sputum sample.
                                                                                                                                                                                                                                                                                                                     The present sequence is that of the Mycobacterium tuberculosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-431611/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shipman R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Antibiotic resistance; rpoB gene; rifampin resistance; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5s
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(ciprofloxacin) and 23S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (VISI-) VISIBLE GENETICS INC
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n), embB (ethambutol), pncA (pyrazinamide),
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
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(azithromycin)
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tuberculosis
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Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                           SIDSI/gcgdata/geneseq/geneseqn-embl/NA1990.DAT:

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   AAX27180
AAS99526
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AAA49823
AAA49825
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                                                                                                                                                                                          Description
                                   RpoB gene
RpoB gene
RpoB gene
RpoB gene
                                                                                                               M. tuberculosis rp
Mycobacterium tube
Mycobacterium tube
 Mycobacterium
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                                   fragment
fragment
fragment
fragment
spec
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Mycobacterium spec	AAS99568	24	306	87.0	17.4	45
	AAS99565	24	306	•	17.4	44
	AAS99560	24	306	•	17.4	4
	AAS99543	24	306	87.0	17.4	42
bacter	AAS99534	24	306	•	17.4	41
gene	AAX27189	19	306	87.0	17.4	40
gene	AAX27186	19	306	•	17.4	39
gene f	AAX27204	19	306	87.0	17.4	38
gene	AAX27198	19	306	87.0	17.4	37
gene	AAX27220	19	306	•	17.4	8
gene	AAX27219	19	306	•	17.4	35
gene	AAX27216	19	306	٠	17.4	4
RpoB gene fragment	AAX27212	19	306	87.0	17.4	w
Mycobacterium tube	AAC88922	22	87	•	18	32
Propionibacterium	AAS59541	23	27426	92.0	œ	ω L
Mycobacterium spec	AAS99557	24	306		18.4	30
bacter	AAS99539	24	306	•	18.4	29
gene	AAX27183	19	306	•	. 8	28
gene	AAX27182	19	306	92.0	18.4	27
gene	AAX27177	19	306	92.0	18.4	26
gene	AAX27196	19	306	•	18.4	25
gene	AAX27193	19	306	•	18.4	24
0	AAX27218	19	306	92.0	18.4	23
M. tuberculosis rp	AAT12091	17	25	٠	8	22
Propionibacterium	AAS59633	23	21500	95.0	19	21
Mycobacterium spec	AAS99551	24	306	95.0	19	20
RpoB gene fragment	AAX27217	19	306	95.0	19	19
_	AAA89994	21	3853	•	20	18
	AAA74651	21	3853	100.0	20	17
	AAH02079	22	3534	100.0	20	16
	AAH51976	22	3519	•	20	, L
	AAT09676	17	970	•	20	14
	AAA49863	21	480	•	20	3
fn.	AAQ61457	14	432	100.0	20	12
spe	AAS99531	24	306	٠	20	11
Mycobacterium spec	9953	24	306	0	20	10

O

ALIGNMENTS

RESULT AAT12092 PR XX PN XXX XXX ACC Antibiotic; resistance; spectrum; gene; mycobacterium; determination; amplification; tuberculosis; rpoB; fragmer primer; differential; hybridisation; pattern; rifampicin; M. tuberculosis rpoB gene fragment amplification primer AAT12092; AAT12092 standard; DNA; 09-JUN-1994; 09-JUN-1995; 14-DEC-1995. Synthetic 10-JUL-1996 rifabutin; species identification; ss. (first entry) 94EP-0870093 95WO-EP02230 20 ВP

P2.

WPI; 1996-040250/04

De Beenhouwer H, Rossau R;

Jannes G,

Machtelinckx L,

Portaels F;

(INNO-) INNOGENETICS NV.

Claim 22; Page 39; 69pp; English. patterns primers for determn. of antibiotic resistance spectrum of ium, opt. coupled with species identification - from patterns of hybridisation with rpoB gene

The antibiotic resistance spectrum (ARS) of a mycobacterium can be determined by amplifying the relevant part of the antibiotic resistance gene, i.e. the M. tuberculosis rpoB gene fragment amplified using the primer set AAT12091-98, hybridising it with a least 1 rpoB gene probe, detecting the hybrids formed and inferring the ARS, and opt. the spp., from the differential hybridisation patterns. The method is partic. useful for the detection of rifampicin and/or rifabutin resistance in M. leprae or M. tuberculosis, and mycobacterial spp. identification. The method is rapid and reliable and provides simultaneous determn. and spp. identity. at be

Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

S Query Match Best Local (Matches Similarity Conservative 100.0%; 0 Score 20; DB 17; Pred. No. 1.6; Mismatches 0 Length 20; 0 Gaps 0,

밁 Н 1 tacggtcggcgagctgatcc 20 tacggtcggcgagctgatcc 20

RESULT AAA49823 Ň

AAA49823 standard; DNA; 20

AAA49823;

25-SEP-2000 (first entry)

Antiblotic resistance; rpoB gene; rifampin resistance; PCR primer; Mycobacterium tuberculosis rpoB gene amplification primer rpoB-F.

Mycobacterium tuberculosis.

WO200036142-A1

22-JUN-2000

10-DEC-1999; 99WO-CA01177.

11-DEC-1998; 98US-0111794.

(VISI-) VISIBLE GENETICS INC.

Shipman

WPI; 2000-431611/37.

Method for the detection and characterization of Mycobacterium tuberculosis with antibiotic resistance in a sample -

Claim 4; Page 4; 43pp; English.

rpoB (rifampin resistance) gene amplification primer rpoB-F (bp 2201-220). It is used with the reverse primer given in AAA49824 and with the sequencing primers given in AAA49825 and AAA49825 for the detection and analysis of antibiotic resistance-associated mutations of the rpoB gene (see AAA49863). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and analysis of antibiotic resistance-associated mutations in defined The present sequence is that of the Mycobacterium tuberculosis of rpoB

> (ciprofloxacin) and 23S (azithromycin) genes of M. tuberculosis. These primers can be used in a method for the detection and characterization of M. tuberculosis present in a sputum sample. The method involves performing a sequencing procedure, with or without prior amplification, to detect the presence of M. tuberculosis, and if present to evaluate the presence of M. tuberculosis, and if present to evaluate the rpoB, katG, rpsL/sl2 and 23S genes for the presence of antibiotic inducing mutations. If M. tuberculosis is detected, a second sequencing procedure is performed on the sample to evaluate additional genes for the presence of antibiotic resistance-inducing mutations. Genotypic tests are rapid, sensitive and accurate providing information as antibiotic treatment outlone. antibiotic treatment options (isoniazid), mabA (isoniazid), rpsL/s12 (streptomycin), (streptomycin), embB (ethambutol), pncA (pyrazinamide), (ciprofloxacin) and 23S (azithromycin) genes of M. tuber rpsL/s12 (streptomycin), 16S/rrs gyrA ç

Sequence 20 BP; 3 A; 6 C; 7 G; 4 T; 0 other;

Matches Query Match Best Local 20; Similarity Conservative 100.0%; 0; Score 20; Pred. No. Mismatches DB 1.6; 0, Length Indels 0, Gaps 0

밁 Ş 20 20

RESULT AAA49825 w

AAA49825 standard; DNA; 20

AAA49825;

25-SEP-2000 (first entry)

Mycobacterium tuberculosis rpoB gene sequencing primer rpoB-5s.

Antibiotic resistance; rpoB gene; rifampin resistance;

Mycobacterium tuberculosis

WO200036142-A1

22-JUN-2000.

10-DEC-1999; 99WO-CA01177

11-DEC-1998; 98US-0111794

(VISI-) VISIBLE GENETICS INC

WPI; 2000-431611/37.

Claim 4; Page 5; 43pp;

The present sequence is that of the Mycobacterium tuberculosis rpoB (rifampin resistance) gene sequencing primer rpoB-5s (bp 2201-2220). It is used with the reverse primer given in AAA49826 and with the amplification primers given in AAA49823 and AAA49826 for the detection and analysis of antibiotic resistance-associated mutations of the rpoB gene (see AAA49863). Amplification and cycle sequencing primers (see AAA49823-62) have been developed for the detection and analysis of antibiotic resistance-associated mutations in defined regions of rpoB (rifampin), katG (isoniazid), oxyR-aphC PR (isoniazid), mabA (isoniazid), rpsL/sl2 (streptomycin), lower control of the detection and regions of mathibotic resistance-associated mutations in defined regions of mathibotic resistance associated mutations and mat (ciprofloxacin) and 23S (azithromycin) genes of (streptomycin), embB (ethambutol), pncA (pyrazinamide),

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Title:
Perfect score:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1: /cgn2_6/ptodate/2/lna/5A_COMB.seq:*
2:, /cgn2_6/ptodate/2/lna/5B_COMB.seq:*
3: /cgn2_6/ptodate/2/lna/6A_COMB.seq:*
4: /cgn2_6/ptodate2/2/lna/6B_COMB.seq:*
5: /cgn2_6/ptodate2/2/lna/PCTUS_COMB.seq:*
6: /cgn2_6/ptodate/2/lna/backfiles1.seq:*
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20
1 tacggcgtttcgat
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Gapop 60.0 , Gapext 60.0
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                   PCT-US95-06790-9
US-08-313-185-57
US-09-082-614A-57
US-09-08-616-169
US-08-906-616-169
US-08-906-616-169
US-09-012-431-169
US-08-906-613-169
US-08-906-613-169
US-08-906-613-171
US-08-906-616-171
US-08-906-616-171
US-08-906-616-171
US-08-906-616-171
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US-08-757-653-136
US-08-757-653-136
US-08-757-653-139
US-08-757-653-140
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Sequence 59, Appl
Sequence 135, App
Sequence 136, App
Sequence 137, App
Sequence 138, App
Sequence 139, App
Sequence 140, App
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57, Appl
169, App
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ddir (rr)			Sequence 20, Appl	Sequence 4, Appli	Sequence 19, Appl	Sequence 19, Appl	Sequence 123, App	Sequence 6, Appli	2	Sequence 64, Appl		Sequence 64, Appl	Sequence 1, Appli	Sequence 1, Appli	Sequence 29, Appl	Sequence 29, Appl	Sequence 29, Appl	Sequence 171, App	

ALIGNMENTS

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Patent No. 5851763; Patent No. 5851763; Patent INFORMATION:
; TOPOLOGY: 1;; MOLECULE TYPE: US-08-313-185-59
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US-08-313-185-59/c
                                                                                                                                                                                             SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/313,185
FILING DATE: 12-OCT-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 02356.0068-00000
TELECOMMUNICATION INFORMATION:
                                                                                                                    INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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APPLICANT: Cole, Stewart
APPLICANT: Young Douglas
APPLICANT: Young Douglas
APPLICANT: Zhang, Ying
APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                   LENGTH: 432 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: Finnegan, Henderson, Farabow, Garrett & ADDRESSEE: Dunner STREET: 1300 I Street, N.W.
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ZIP: 20005-3315
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                 DNA (genomic)
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RESULT 2
US-09-082-614A-59/c
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US-08-757-653-135/c
; Sequence 135, Application US/08757653
; Patent No. 5843669
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                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                  Matches
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                                                                                       428 TACGGCGTTTCGATGAACCC 409
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                                   1 tacggcgtttcgatgaaccc
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.ICANT: Telenti, Amalio
.ICANT: Bedmer, Thomas
LE OF INVENTION: Rapid Detection of Antibiotic Resistance
LE OF INVENTION: in Mycobacterium Tuberculosis
LER OF SEQUENCES: 66
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1300 I Street, N.W
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Cole, Stewart
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Zhang, Ying
                                                                                                                                                  Conservative
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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linear
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; Mismatches 0;
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Pred. No. 0.00054;
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Sequence 136, App.
Sequence 136, App.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: FO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION: NAME: Ingolia, Diane E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                        APPLICANT: Kaiser, APPLICANT: Lyamiche APPLICANT: Lyamiche
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                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                    IITLE OF INVENTION: Cleavage Of Nucleic Acid Using
IITLE OF INVENTION: Thermostable FEN-1 Endonucleases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          296 TACGGCGTTTCGATGAACCC 277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Ingolia, Diane REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/757,653 FILING DATE:
                                                                                                                                              STREET: 240 ...
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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Lyamichev, Natasha
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                                                                                                                           United States Of America
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Pred. No.
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Maximum DB
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,
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3: /cgn2_6/ptodata/2
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-08-750-030-1
US-08-750-030-9
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US-08-250-030-9
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US-08-313-185-57
US-09-012-614A-57
US-09-012-63-169
US-08-906-769-169
US-08-906-769-169
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Sequence 137, Appl
Sequence 138, Appl
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ALIGNMENTS	US-08-998-416-615	US-08-282-696-20	US-08-459-586-20	PCT-US96-04648-4	US-08-282-696-19	US-08-459-586-19	US-08-976-259-123	US-08-636-928-6	US-09-103-840A-2	US-09-232-201-64	US-09-232-197-64	US-09-232-200-64	US-09-360-682A-1	US-08-896-344A-1	us-09-232-201-29	US-09-232-197-29	US-09-232-200-29	US-08-906-613-171	
	615	Sequence 20, Appl	Sequence 20, Appl	Sequence 4, Appli	Sequence 19, Appl	Sequence 19, Appl	Sequence 123, App	Sequence 6, Appli	Sequence 2, Appli	Sequence 64, Appl	Sequence 64, Appl	Sequence 64, Appl	Sequence 1, Appli	1,	Sequence 29, Appl		Sequence 29, Appl	Sequence 171, App	

US-08-313-185-59/c Application US/08313185

Sequence

Patent No. GENERAL I APPLICANT: Honore, Nadine
APPLICANT: Telenti, Amalio
APPLICANT: Bodner, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66 CORRESPONDENCE ADDRESS: STREET: 1300 I STATE: Washington ADDRESSEE: Finnegan, Henderson, ADDRESSEE: Dunner STREET: 1300 I Street, N.W. 59, 585176 585176 INFORMATION: Heym, Beate Cole, Stewart Young, Douglas Zhang, Ying Farabow, Garrett &

STRANDEDNESS: single;
TOPOLOGY: linear;
MOLECULE TYPE: DNA (ger US-08-313-185-59 NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 0235/
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEPAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 base pairs
TYPE: nucleic acid COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: ATTORNEY/AGENT INFORMATION: APPLICATION NUMBER: US/08/313,185 FILING DATE: 12-OCT-1994 CLASSIFICATION: 435 COUNTRY: USA ZIP: 20005-3315 DNA (genomic) 02356.0068-00000

Query Match

100.0%; Score 20; DB 2. Length 432;

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RESULT 3
US-08-757-653-135/c
; Sequence 135, Application US/08757653
; Patent No. 5843669
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; MOLECULE TYPE:
US-09-082-614A-59
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                                                                                                                                                       Matches
                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                              TELEFAX: (202) 408-44 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 12-OCT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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APPLICANT: Telenti, Amalio
APPLICANT: Bodmer, Thomas
TITLE OF INVENTION: Rapid Detection of Antibiotic Resistance
TITLE OF INVENTION: in Mycobacterium Tuberculosis
NUMBER OF SEQUENCES: 66
                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 02356.0068-00000
                                                                                                                                                                                                                                                                                STRANDEDNESS:
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                                                                                                             1 tacggcgtttcgatgaaccc 20
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Zhang, Ying
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Cole, Stewart
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408-3400
409: 59:
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Pred. No. 0.00054;
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                                                                                                                                                                                    Length 432;
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; MOLECULE TYPE:
US-08-757-653-135
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                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Kaiser,
APPLICANT: Lyamich
APPLICANT: Lyamich
                                                                                                                                                                                                                                                                                                                          Patent No.
                                                                                                                                                                                                                                                                                                                                       Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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APPLICANT: Lyamichev, Natasha
TITLE OF INVENTION: Cleavage Of Nucleic Acid Using
TITLE OF INVENTION: Thermostable FEN-1 Endonucleas
                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                      296 TACGGCGTTTCGATGAACCC
                          MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: FO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0,
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Medien & ....
STREET: 220 Montgomery Street,
                                                                                                           COUNTRY:
                                                                                                                                            CITY: San Francisco
                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 620 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER:
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20; Conserv
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ARE: PatentIn Release #1.0, APPLICATION DATA:
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                                                                                                                             California
                                                                                                                                                         220 Montgomery
                                                                                                                                                                                                                                                                                                                                       Application US/08757653
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                                                                                                                                                                                                                                                                    Kaiser, Michael W.
Lyamichev, Victor I.
                                                                                                           United States
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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Medlen & Carroll, LLP
Medlen & Street, Suite 2200
                                                                                                                                                                            Medlen & Carroll,
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Thermostable FEN-1 Endonucleases
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Pred. No. 0.00054;
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               Version #1.30
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